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9/B

IM-5.ST25.txt
SEQUENCE LISTING

<110> Wonderling, Ramani S.
Boroughs, Karen L.

<120> CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
THEREOF

<130> IM-5

<140> 09/917,265
<141> 2001-07-27

<150> 60/223,016
<151> 2000-08-04

<160> 111

<170> PatentIn version 3.2

<210> 1
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<212> DNA
<213> Felis catus

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<220>
<221> misc_feature
<222> (470)..(470)
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aaaccttcca gatcccttcc tctcttagga aactattgag cacagggata aag atg 116
Met
1
act gct ata cca gta gat gat tgc atc aac ttt gtg gga atg aaa ttt 164
Thr Ala Ile Pro Val Asp Asp Cys Ile Asn Phe Val Gly Met Lys Phe
5 10 15
att gac aat aca ctt tac ttt gta gct gac agt gat gaa aac ctg gaa 212
Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu Glu
20 25 30
aca gat tac ttt ggc aag ctt gaa cat aaa ctc tca atc tta cga aac 260
Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn
35 40 45
ttg aac gac caa gtt ctc ttc att aac cag gga gat caa cct gtg ttt 308
Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe
50 55 60 65

IM-5.ST25.txt

gag gat atg cct gat tct gac tgt aca gat aat gca ccc cgg act gaa 356
Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu
70 75 80

ttt atc ata tat atg tat aaa gat agc ctc act aga ggt ctg gca gta 404
Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val
85 90 95

acc atc tct gtg aat tat aag acc atg tct act ctc tcc tgt gag aac 452
Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn
100 105 110

aaa att att tcc ttt aan gga atg agt cct cct gag agt atc aat gat 500
Lys Ile Ile Ser Phe Xaa Gly Met Ser Pro Pro Glu Ser Ile Asn Asp
115 120 125

gaa gga aat gac at 514
Glu Gly Asn Asp
130

<210> 2
<211> 133
<212> PRT
<213> Felis catus

<220>
<221> misc_feature
<222> (119)..(119)
<223> The 'Xaa' at location 119 stands for Lys, or Asn.

<400> 2

Met Thr Ala Ile Pro Val Asp Asp Cys Ile Asn Phe Val Gly Met Lys
1 5 10 15

Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu
20 25 30

Glu Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg
35 40 45

Asn Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val
50 55 60

Phe Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr
65 70 75 80

Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala
85 90 95

Val Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu
100 105 110

IM-5.ST25.txt

Asn Lys Ile Ile Ser Phe Xaa Gly Met Ser Pro Pro Glu Ser Ile Asn
 115 120 125

Asp Glu Gly Asn Asp
 130

<210> 3
 <211> 514
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 ttgtttctcac aggagagagt agacatgggtc ttataattca cagagatggg tactgccaga 120
 cctctagtga ggctatcttt atacatatat atgataaatt cagtccgggg tgcattatct 180
 gtacagtcag aatcaggcat atcctcaaac acaggttgat ctccctgggt aatgaagaga 240
 acttggtcgt tcaagtttcg taagattgag agtttatgtt caagcttgcc aaagtaatct 300
 gtttccagggt tttcatcact gtcagctaca aagtaaagtg tattgtcaat aaatttcatt 360
 cccacaaagt tgatgcaatc atctactggg atagcagtca tctttatccc tgtgctcaat 420
 agtttcctaa gagaggaagg gatctggaag gtttgagggt cctttctttt cctgagctgt 480
 gtagatggca gaaggtggca ggagcgctt tagc 514

<210> 4
 <211> 502
 <212> DNA
 <213> Felis catus

<220>
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 <222> (3)..(464)

<220>
 <221> misc_feature
 <222> (126)..(126)
 <223> n = unknown at position 126
 Xaa = unknown at position 42

<400> 4
 gc aag ctt gaa cat aaa ctc tca atc tta cga aac ttg aac gac caa 47

IM-5.ST25.txt

Lys	Leu	Glu	His	Lys	Leu	Ser	Ile	Leu	Arg	Asn	Leu	Asn	Asp	Gln		
1				5				10						15		
gtt	ctc	ttc	att	aac	cag	gga	gat	caa	cct	gtg	ttt	gag	gat	atg	cct	95
Val	Leu	Phe	Ile	Asn	Gln	Gly	Asp	Gln	Pro	Val	Phe	Glu	Asp	Met	Pro	
				20				25						30		
gat	tct	gac	tgt	aca	gat	aat	gca	ccc	cgg	nct	gaa	ttt	atc	ata	tat	143
Asp	Ser	Asp	Cys	Thr	Asp	Asn	Ala	Pro	Arg	Xaa	Glu	Phe	Ile	Ile	Tyr	
			35				40						45			
atg	tat	aaa	gat	agc	ctc	act	aga	ggg	ctg	gca	gta	acc	atc	tct	gtg	191
Met	Tyr	Lys	Asp	Ser	Leu	Thr	Arg	Gly	Leu	Ala	Val	Thr	Ile	Ser	Val	
		50					55					60				
aat	tat	aag	acc	atg	tct	act	ctc	tcc	tgt	gag	aac	aaa	att	att	tcc	239
Asn	Tyr	Lys	Thr	Met	Ser	Thr	Leu	Ser	Cys	Glu	Asn	Lys	Ile	Ile	Ser	
	65					70					75					
ttt	aag	gaa	atg	agt	cct	cct	gag	agt	atc	aat	gat	gaa	gga	aat	gac	287
Phe	Lys	Glu	Met	Ser	Pro	Pro	Glu	Ser	Ile	Asn	Asp	Glu	Gly	Asn	Asp	
80					85				90					95		
atc	ata	ttc	ttt	cag	aga	agt	gtt	cca	gga	cat	gat	gat	aag	ata	caa	335
Ile	Ile	Phe	Phe	Gln	Arg	Ser	Val	Pro	Gly	His	Asp	Asp	Lys	Ile	Gln	
				100				105						110		
ttt	gag	tct	tca	ttg	tac	aag	ggg	tac	ttt	cta	gct	tgt	gaa	aaa	gag	383
Phe	Glu	Ser	Ser	Leu	Tyr	Lys	Gly	Tyr	Phe	Leu	Ala	Cys	Glu	Lys	Glu	
			115				120						125			
aaa	gat	ctt	ttc	aaa	ctc	att	ttg	aaa	aaa	aag	gat	gaa	aat	ggg	gat	431
Lys	Asp	Leu	Phe	Lys	Leu	Ile	Leu	Lys	Lys	Lys	Asp	Glu	Asn	Gly	Asp	
		130					135					140				
aag	tcc	ata	atg	ttc	act	gtt	caa	aac	aag	aat	tagatattaa	aattgcataa				484
Lys	Ser	Ile	Met	Phe	Thr	Val	Gln	Asn	Lys	Asn						
	145					150										
tttgaaaaaa	aaaaaaaa															502

<210> 5
 <211> 154
 <212> PRT
 <213> Felis catus

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 <222> (42)..(42)
 <223> The 'Xaa' at location 42 stands for Thr, Ala, Pro, or Ser.

<400> 5

Lys	Leu	Glu	His	Lys	Leu	Ser	Ile	Leu	Arg	Asn	Leu	Asn	Asp	Gln	Val
1				5				10						15	

Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro Asp

Ser Asp Cys Thr Asp Asn Ala Pro Arg Xaa Glu Phe Ile Ile Tyr Met
35 40 45

Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val Asn
50 55 60

Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe
65 70 75 80

Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp Ile
85 90 95

Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln Phe
100 105 110

Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu Lys
115 120 125

Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp Lys
130 135 140

Ser Ile Met Phe Thr Val Gln Asn Lys Asn
145 150

<210> 6
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<213> Felis catus

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<222> (377)..(377)
<223> n = unknown at position 377

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attatggact tatccccatt ttcattccttt tttttcaaaa tgagtttgaa aagatctttc 120
tctttttcac aagctagaaa gtacccttg tacaatgaag actcaaattg tatcttatca 180
tcatgtcctg gaacacttct ctgaaagaat atgatgtcat ttccttcac attgatactc 240
tcaggaggac tcatttcctt aaaggaaata attttggttct cacaggagag agtagacatg 300
gtcttataat tcacagagat gggttactgcc agacctctag tgaggctatc ttatatacata 360

tatatgataa attcagnccg ggggtgcatta tctgtacagt cagaatcagg catatcctca	420
aacacagggtt gatctccctg gttaatgaag agaacttggt cgttcaagtt tcgtaagatt	480
gagagtttat gttcaagctt gc	502

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<220>
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<222> (24) .. (599)
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IM-5.ST25.txt

Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu Lys Asp Leu Phe Lys
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 ctc att ttg aaa aaa aag gat gaa aat ggg gat aag tcc ata atg ttc 581
 Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp Lys Ser Ile Met Phe
 175 180 185

 act gtt caa aac aag aat tagatatt 607
 Thr Val Gln Asn Lys Asn
 190

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 <211> 192
 <212> PRT
 <213> Felis catus

 <400> 8

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 20 25 30

 Glu Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg
 35 40 45

 Asn Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val
 50 55 60

 Phe Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr
 65 70 75 80

 Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala
 85 90 95

 Val Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu
 100 105 110

 Asn Lys Ile Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn
 115 120 125

 Asp Glu Gly Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His
 130 135 140

 Asp Asp Lys Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu
 145 150 155 160

IM-5.ST25.txt

Ala Cys Glu Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys
 165 170 175

Asp Glu Asn Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn
 180 185 190

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 <212> DNA
 <213> Felis catus

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 gaacataaac tctcaatctt acgaaacttg aacgaccaag ttctcttcat taaccaggga 180
 gatcaacctg tgtttgagga tatgcctgat tctgactgta cagataatgc accccggact 240
 gaatttatca tatatatgta taaagatagc ctactagag gtctggcagt aaccatctct 300
 gtgaattata agaccatgtc tactctctcc tgtgagaaca aaattatttc ctttaaggaa 360
 atgagtcctc ctgagagtat caatgatgaa ggaaatgaca tcatattctt tcagagaagt 420
 gttccaggac atgatgataa gatacaattt gagtcttcat tgtacaaggg gtactttcta 480
 gcttgatgaa aagagaaaga tcttttcaaa ctcatatttg aaaaaagga tgaaaatggg 540
 gataagtcca taatgttcac tgttcaaac aagaat 576

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 tacaatgaag actcaaattg tatcttatca tcatgtcctg gaacacttct ctgaaagaat 180
 atgatgtcat ttccttcac attgatactc tcaggaggac tcatttcctt aaaggaaata 240
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 tctgtacagt cagaatcagg catatcctca aacacagggt gatctccctg gttaatgaag 420
 agaacttggc cgttcaagtt tcgtaagatt gagagtttat gttcaagctt gccaaagtaa 480
 tctgtttcca ggttttcac actgtcagct acaaagtaaa gtgtattgtc aataaatttc 540

IM-5.ST25.txt

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<211> 471
<212> DNA
<213> Felis catus

<220>
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<222> (1)..(471)

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1 5 10 15
gac caa gtt ctc ttc att aac cag gga gat caa cct gtg ttt gag gat 96
Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp
20 25 30
atg cct gat tct gac tgt aca gat aat gca ccc cgg act gaa ttt atc 144
Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu Phe Ile
35 40 45
ata tat atg tat aaa gat agc ctc act aga ggt ctg gca gta acc atc 192
Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile
50 55 60
tct gtg aat tat aag acc atg tct act ctc tcc tgt gag aac aaa att 240
Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile
65 70 75 80
att tcc ttt aag gaa atg agt cct cct gag agt atc aat gat gaa gga 288
Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly
85 90 95
aat gac atc ata ttc ttt cag aga agt gtt cca gga cat gat gat aag 336
Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys
100 105 110
ata caa ttt gag tct tca ttg tac aag ggg tac ttt cta gct tgt gaa 384
Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu
115 120 125
aaa gag aaa gat ctt ttc aaa ctc att ttg aaa aaa aag gat gaa aat 432
Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn
130 135 140
ggg gat aag tcc ata atg ttc act gtt caa aac aag aat 471
Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn
145 150 155

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<211> 157

IM-5.ST25.txt

<212> PRT

<213> Felis catus

<400> 12

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20 25 30

Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu Phe Ile
35 40 45

Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile
50 55 60

Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile
65 70 75 80

Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly
85 90 95

Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys
100 105 110

Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu
115 120 125

Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn
130 135 140

Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn
145 150 155

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<212> DNA

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agactcaa atgtatcttat catcatgtcc tggaacactt ctctgaaaga atatgatgtc 180
atttccttca tcattgatac tctcaggagg actcatttcc ttaaaggaaa taattttggt 240

IM-5.ST25.txt

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 agtgaggcta tctttataca tatatatgat aaattcagtc cggggtgcat tatctgtaca 360
 gtcagaatca ggcataatcct caaacacagg ttgatctccc tgggttaatga agagaacttg 420
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 <222> (1)..(1230)

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 1 5 10 15
 gtc ggc atg ggg acg gtc aac ggc ttg ctg gat gaa ctc ttt gag aaa 96
 Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys
 20 25 30
 aac gtg ctg aac cag gag gag atg gag aga gta aaa tgt gaa aac gct 144
 Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala
 35 40 45
 acc gtt atg gac aag gcc cga gct ctg atc gac agc gtc ctg cgg aaa 192
 Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys
 50 55 60
 ggg cca cgg gcg tgc cag atc ttt atc tgt cac atc tgt gag gaa gac 240
 Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp
 65 70 75 80
 acc cac ctt gca gag acg ctg ggg ctc tcc tca agc cca caa tct gga 288
 Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly
 85 90 95
 aat tct cag aac acc acg gac tct gaa gta gcg ttt cct cct ctt cca 336
 Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro
 100 105 110
 gcc agc gtg aat aac atg cct ggg ccg gct gag cca gaa gaa tct gta 384
 Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val
 115 120 125
 gat gct ctc aag ctt tgt cct cgt gaa aac ttc gtg aaa ctg tgt aaa 432
 Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys
 130 135 140
 cag agg gct gaa gag atc tac cca ata aag gag aga aag gat cgt act 480
 Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr
 145 150 155 160

IM-5.ST25.txt

cgt ctg gct ctc atc ata tgc aat acg acg ttc gat cat ctt tct ctc	528
Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu	
165 170 175	
agg aag ggg gct gac ctt gac gtt gca ggg atg agg agg ctg ctt aca	576
Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr	
180 185 190	
gac ctt ggc tac agt gtg cac ata aaa gag gaa ctc act gct aag gac	624
Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp	
195 200 205	
atg gaa tca gag ctg agg gca ttt gct gcc cgt cca gag cac aag tcc	672
Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser	
210 215 220	
tcg gac agc aca ttc ctg gtg ttc atg tct cat ggc atc ctg agt gga	720
Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly	
225 230 235 240	
atc tgt ggg acg aag tac agc gct gaa gga gac cca gat gta ttg gct	768
Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala	
245 250 255	
tat gac acc atc ttc cag att ttc aac aac cgc aac tgc ctt agt cta	816
Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu	
260 265 270	
aag gac aag ccc aag gtc atc atc gtc cag gcc tgc aga ggt gaa aat	864
Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn	
275 280 285	
ttg ggg gaa ctg ttg atc agt gac tct cca gcg gcc cca atg gac agc	912
Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser	
290 295 300	
act tca cag atg ggt agc agc ctt tca cag gtg ggt gac aac cta gag	960
Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu	
305 310 315 320	
gac gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc	1008
Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe	
325 330 335	
tgc tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga	1056
Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly	
340 345 350	
tct ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg	1104
Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp	
355 360 365	
tgc ttt cat ctg gag gaa gta ttt cgg aag gta caa cag tca ttt gaa	1152
Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu	
370 375 380	
aaa cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg	1200
Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met	

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IM-5.ST25.txt
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Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala
                               35                               40                               45
Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys
                               50                               55                               60
Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp
65                               70                               75                               80
Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly
                               85                               90                               95
Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro
                               100                               105                               110
Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val
                               115                               120                               125
Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys
                               130                               135                               140
Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr
145                               150                               155                               160
Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu
                               165                               170                               175
Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr

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180		185		190											
Asp	Leu	Gly	Tyr	Ser	Val	His	Ile	Lys	Glu	Glu	Leu	Thr	Ala	Lys	Asp
195							200					205			
Met	Glu	Ser	Glu	Leu	Arg	Ala	Phe	Ala	Ala	Arg	Pro	Glu	His	Lys	Ser
210						215					220				
Ser	Asp	Ser	Thr	Phe	Leu	Val	Phe	Met	Ser	His	Gly	Ile	Leu	Ser	Gly
225					230					235					240
Ile	Cys	Gly	Thr	Lys	Tyr	Ser	Ala	Glu	Gly	Asp	Pro	Asp	Val	Leu	Ala
				245					250					255	
Tyr	Asp	Thr	Ile	Phe	Gln	Ile	Phe	Asn	Asn	Arg	Asn	Cys	Leu	Ser	Leu
			260					265					270		
Lys	Asp	Lys	Pro	Lys	Val	Ile	Ile	Val	Gln	Ala	Cys	Arg	Gly	Glu	Asn
		275					280					285			
Leu	Gly	Glu	Leu	Leu	Ile	Ser	Asp	Ser	Pro	Ala	Ala	Pro	Met	Asp	Ser
	290					295					300				
Thr	Ser	Gln	Met	Gly	Ser	Ser	Leu	Ser	Gln	Val	Gly	Asp	Asn	Leu	Glu
305					310					315					320
Asp	Asp	Ala	Ile	Tyr	Lys	Val	His	Val	Glu	Lys	Asp	Phe	Ile	Ala	Phe
				325					330					335	
Cys	Ser	Ser	Thr	Pro	His	His	Val	Ser	Trp	Arg	Asp	Val	Asn	Lys	Gly
			340					345					350		
Ser	Leu	Phe	Ile	Thr	Gln	Leu	Ile	Thr	Cys	Phe	Gln	Lys	Tyr	Ser	Trp
		355					360					365			
Cys	Phe	His	Leu	Glu	Glu	Val	Phe	Arg	Lys	Val	Gln	Gln	Ser	Phe	Glu
	370					375					380				
Lys	Pro	Asn	Val	Arg	Ala	Gln	Met	Pro	Thr	Ile	Glu	Arg	Leu	Ser	Met
385					390					395					400
Thr	Arg	Cys	Phe	Tyr	Leu	Phe	Pro	Gly	His						
				405					410						

IM-5.ST25.txt

<210> 16
 <211> 1233
 <212> DNA
 <213> Felis catus

<400> 16
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 ctgggctcta acatttggtt tttcaaataga ctgttgtacc ttccgaaata cttcctccag 120
 atgaaagcac cacgaatact tttggaagca cgtgatgagt tgtgtaataga agagagatcc 180
 cttgttcacg tctctccaag acacatgatg tggggctcgag gagcagaaag cgatgaagtc 240
 cttctccacg tggaccttgt aaatggcgct gtccctctagg ttgtcaccca cctgtgaaag 300
 gctgctaccc atctgtgaag tgctgtccat tggggccgct ggagagtcac tgatcaacag 360
 ttccccaaa ttttcacctc tgcaggcctg gacgatgatg accttgggct tgtcctttag 420
 actaaggcag ttgcggttgt tgaaaatctg gaagatgggtg tcataagcca atacatctgg 480
 gtctccttca gcgctgtact tegtcccaca gattccactc aggatgccat gagacatgaa 540
 caccaggaat gtgctgtccg aggacttggt ctctggacgg gcagcaaag ccctcagctc 600
 tgattccatg tccttagcag tgagttcctc ttttatgtgc aactgtagc caaggctctgt 660
 aagcagcctc ctcatccctg caacgtcaag gtcagcccc ttcttgagag aaagatgatc 720
 gaacgtcgta ttgcatatga tgagagccag acgagtacga tcctttctct cctttattgg 780
 gtagatctct tcagccctct gtttacacag tttcacgaag ttttcacgag gacaaagctt 840
 gagagcatct acagattctt ctggctcagc cggcccaggc atgttattca cgctggctgg 900
 aagaggagga aacgctactt cagagtccgt ggtgttctga gaatttccag attgtgggct 960
 tgaggagagc cccagcgtct ctgcaagggt ggtgtcttcc tcacagatgt gacagataaa 1020
 gatctggcac gcccggtggc ctttccgcag gacgctgtcg atcagagctc gggccttgtc 1080
 cataacggta gcgttttcac attttactct ctccatctcc tcttgggtta gcacgttttt 1140
 ctcaaagagt tcatccagca agccgttgac cgtcccatg ccgactgagt tgatgaactg 1200
 cttcctcttc tccttcagga ccttgctcggc cat 1233

<210> 17
 <211> 526
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (18) .. (524)

IM-5.ST25.txt

<400> 17
 ggcacgagca aaaagcc atg gcc gac aag gat ctg aag ggc aag agg aag 50
 Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys
 1 5 10

cag ttc atc aac tca gtc ggc atg ggg acg gtc aac ggc ttg ctg gat 98
 Gln Phe Ile Asn Ser Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp
 15 20 25

gaa ctc ttt gag aaa aac gtg ctg aac cag gag gag atg gag aga gta 146
 Glu Leu Phe Glu Lys Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val
 30 35 40

aaa tgt gaa aac gct acc gtt atg gac aag gcc cga gct ctg atc gac 194
 Lys Cys Glu Asn Ala Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp
 45 50 55

agc gtc ctg cgg aaa ggg cca cgg gcg tgc cag atc ttt atc tgt cac 242
 Ser Val Leu Arg Lys Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His
 60 65 70 75

atc tgt gag gaa gac acc cac ctt gca gag acg ctg ggg ctc tcc tca 290
 Ile Cys Glu Glu Asp Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser
 80 85 90

agc cca caa tct gga aat tct cag aac acc acg gac tct gaa gta gcg 338
 Ser Pro Gln Ser Gly Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala
 95 100 105

ttt cct cct ctt cca gcc agc gtg aat aac atg cct ggg ccg gct gag 386
 Phe Pro Pro Leu Pro Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu
 110 115 120

cca gaa gaa tct gta gat gct ctc aag ctt tgt cct cgt gaa aac ttc 434
 Pro Glu Glu Ser Val Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe
 125 130 135

gtg aaa ctg tgt aaa cag agg gct gaa gag atc tac cca ata aag gag 482
 Val Lys Leu Cys Lys Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu
 140 145 150 155

aga aag gat cgt act cgt ctg gct ctc atc ata tgc aat acg ac 526
 Arg Lys Asp Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Thr
 160 165

<210> 18
 <211> 169
 <212> PRT
 <213> Felis catus

<400> 18
 Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys Gln Phe Ile Asn Ser
 1 5 10 15

Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys
 20 25 30

IM-5.ST25.txt

Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala
35 40 45

Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys
50 55 60

Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp
65 70 75 80

Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly
85 90 95

Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro
100 105 110

Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val
115 120 125

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys
130 135 140

Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr
145 150 155 160

Arg Leu Ala Leu Ile Ile Cys Asn Thr
165

<210> 19
<211> 526
<212> DNA
<213> Felis catus

<400> 19
gtcgtattgc atatgatgag agccagacga gtacgatacct ttctctcctt tattgggtag 60
atctcttcag ccctctgttt acacagtttc acgaagtttt cagcaggaca aagcttgaga 120
gcatctacag attcttcttg ctcagccggc ccaggcatgt tattcacgct ggctggaaga 180
ggaggaaacg ctacttcaga gtccgtggtg ttctgagaat ttccagattg tgggcttgag 240
gagagcccca gcgtctctgc aagggtgggtg tcttctcac agatgtgaca gataaagatc 300
tggcacgccc gtggcccttt ccgcaggacg ctgtcgatca gagctcgggc cttgtccata 360
acggtagcgt tttcacattt tactctctcc atctctcct gggtcagcac gtttttctca 420
aagagttcat ccagcaagcc gttgaccgtc cccatgccga ctgagttgat gaactgcttc 480

ctctttgccct tcagatcctt gtcggccatg gcttttttgct cgtgcc 526

<210> 20
 <211> 500
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (3)..(362)

<220>
 <221> misc_feature
 <222> (473)..(473)
 <223> n = unknown at position 473

<400> 20
 gg gaa ctg ttg atc agt gac tct cca gcg gcc cca atg gac agc act 47
 Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser Thr
 1 5 10 15

tca cag atg ggt agc agc ctt tca cag gtg ggt gac aac cta gag gac 95
 Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu Asp
 20 25 30

gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc tgc 143
 Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe Cys
 35 40 45

tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga tct 191
 Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly Ser
 50 55 60

ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg tgc 239
 Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp Cys
 65 70 75

ttt cat ctg gag gaa gta ttt cgg aag gta caa cag tca ttt gaa aaa 287
 Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Lys
 80 85 90 95

cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg aca 335
 Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met Thr
 100 105 110

aga tac ttc tat ctc ttc cct ggc aat tgaaaatagc aatcatgggc 382
 Arg Tyr Phe Tyr Leu Phe Pro Gly Asn
 115 120

agtccagccc ttcttgacca acttggaataa gtaccttagc tagcacaaca cactcattta 442

acgtttggtta tctcaataaaa aatgaaaaca nctaaaaaaaa aaaaaaaaaa aaaaaaaaaa 500

<210> 21
 <211> 120

<212> PRT

<213> Felis catus

<400> 21

Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser Thr Ser
 1 5 10 15

Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu Asp Asp
 20 25 30

Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe Cys Ser
 35 40 45

Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly Ser Leu
 50 55 60

Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp Cys Phe
 65 70 75 80

His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Lys Pro
 85 90 95

Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met Thr Arg
 100 105 110

Tyr Phe Tyr Leu Phe Pro Gly Asn
 115 120

<210> 22

<211> 500

<212> DNA

<213> Felis catus

<220>

<221> misc_feature

<222> (28)..(28)

<223> n = unknown at position 28

<400> 22

tttttttttt tttttttttt ttttttagntg ttttcatttt tattgagata ccaaacttta 60

aatgagtgtg ttgtgctagc taaggacttt ttccaagttg gtcaagaagg gctggactgc 120

ccatgattgc ttttttcaat tgccagggaa gagatagaag tatcttgtca tggatagtcg 180

ttcaatggtg ggcattctggg ctctaactt tggtttttca aatgactggt gtaccttccg 240

aaatacttcc tccagatgaa agcaccacga atacttttgg aagcacgtga tgagttgtgt 300

IM-5.ST25.txt

aatgaagaga gatcccttgt tcacgtctct ccaagacaca tgatgtgggg tcgaggagca 360
gaaagcgatg aagtccttct ccacgtggac cttgtaaatg gcgtcgtcct ctaggttgtc 420
acccacctgt gaaaggctgc taccatctg tgaagtgtg tccattgggg ccgctggaga 480
gtcactgac aacagttccc 500

<210> 23
<211> 1230
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (1)..(1230)

<400> 23
atg gcc gac aag gat ctg aag ggc aag agg aag cag ttc atc aac tca 48
Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys Gln Phe Ile Asn Ser
1 5 10 15
gtc ggc atg ggg acg gtc aac ggc ttg ctg gat gaa ctc ttt gag aaa 96
Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys
20 25 30
aac gtg ctg aac cag gag gag atg gag aga gta aaa tgt gaa aac gct 144
Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala
35 40 45
acc gtt atg gac aag gcc cga gct ctg atc gac agc gtc ctg cgg aaa 192
Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys
50 55 60
ggg cca cgg gcg tgc cag atc ttt atc tgt cac atc tgt gag gaa gac 240
Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp
65 70 75 80
acc cac ctt gca gag acg ctg ggg ctc tcc tca agc cca caa tct gga 288
Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly
85 90 95
aat tct cag aac acc acg gac tct gaa gta gcg ttt cct cct ctt cca 336
Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro
100 105 110
gcc agc gtg aat aac atg cct ggg ccg gct gag cca gaa gaa tct gta 384
Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val
115 120 125
gat gct ctc aag ctt tgt cct cgt gaa aac ttc gtg aaa ctg tgt aaa 432
Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys
130 135 140
cag agg gct gaa gag atc tac cca ata aag gag aga aag gat cgt act 480
Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr
145 150 155 160

IM-5.ST25.txt

cgt ctg gct ctc atc ata tgc aat acg acg ttc gat cat ctt tct ctc	528
Arg Leu Ala Leu Ile Ile Cys Asn Thr Phe Asp His Leu Ser Leu	
165 170 175	
agg aag ggg gct gac ctt gac gtt gca ggg atg agg agg ctg ctt aca	576
Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr	
180 185 190	
gac ctt ggc tac agt gtg cac ata aaa gag gaa ctc act gct aag gac	624
Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp	
195 200 205	
atg gaa tca gag ctg agg gca ttt gct gcc cgt cca gag cac aag tcc	672
Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser	
210 215 220	
tcg gac agc aca ttc ctg gtg ttc atg tct cat ggc atc ctg agt gga	720
Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly	
225 230 235 240	
atc tgt ggg acg aag tac agc gct gaa gga gac cca gat gta ttg gct	768
Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala	
245 250 255	
tat gac acc atc ttc cag att ttc aac aac cgc aac tgc ctt agt cta	816
Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu	
260 265 270	
aag gac aag ccc aag gtc atc atc gtc cag gcc tgc aga ggt gaa aat	864
Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn	
275 280 285	
ttg ggg gaa ctg ttg atc agt gac tct cca gcg gcc cca atg gac agc	912
Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser	
290 295 300	
act tca cag atg ggt agc agc ctt tca cag gtg ggt gac aac cta gag	960
Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu	
305 310 315 320	
gac gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc	1008
Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe	
325 330 335	
tgc tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga	1056
Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly	
340 345 350	
tct ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg	1104
Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp	
355 360 365	
tgc ttt cat ctg gag gaa gta ttt cgg aag gta caa cag tca ttt gaa	1152
Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu	
370 375 380	
aaa cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg	1200
Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met	

385

390

395

400

aca aga tac ttc tat ctc ttc cct ggc aat
 Thr Arg Tyr Phe Tyr Leu Phe Pro Gly Asn
 405 410

1230

<210> 24

<211> 410

<212> PRT

<213> Felis catus

<400> 24

Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys Gln Phe Ile Asn Ser
 1 5 10 15

Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys
 20 25 30

Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala
 35 40 45

Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys
 50 55 60

Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp
 65 70 75 80

Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly
 85 90 95

Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro
 100 105 110

Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val
 115 120 125

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys
 130 135 140

Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr
 145 150 155 160

Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu
 165 170 175

Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr

180		185		190											
Asp	Leu	Gly	Tyr	Ser	Val	His	Ile	Lys	Glu	Glu	Leu	Thr	Ala	Lys	Asp
	195						200					205			
Met	Glu	Ser	Glu	Leu	Arg	Ala	Phe	Ala	Ala	Arg	Pro	Glu	His	Lys	Ser
	210					215					220				
Ser	Asp	Ser	Thr	Phe	Leu	Val	Phe	Met	Ser	His	Gly	Ile	Leu	Ser	Gly
225					230					235					240
Ile	Cys	Gly	Thr	Lys	Tyr	Ser	Ala	Glu	Gly	Asp	Pro	Asp	Val	Leu	Ala
				245					250					255	
Tyr	Asp	Thr	Ile	Phe	Gln	Ile	Phe	Asn	Asn	Arg	Asn	Cys	Leu	Ser	Leu
			260					265					270		
Lys	Asp	Lys	Pro	Lys	Val	Ile	Ile	Val	Gln	Ala	Cys	Arg	Gly	Glu	Asn
		275					280					285			
Leu	Gly	Glu	Leu	Leu	Ile	Ser	Asp	Ser	Pro	Ala	Ala	Pro	Met	Asp	Ser
	290					295					300				
Thr	Ser	Gln	Met	Gly	Ser	Ser	Leu	Ser	Gln	Val	Gly	Asp	Asn	Leu	Glu
305					310					315				320	
Asp	Asp	Ala	Ile	Tyr	Lys	Val	His	Val	Glu	Lys	Asp	Phe	Ile	Ala	Phe
				325					330					335	
Cys	Ser	Ser	Thr	Pro	His	His	Val	Ser	Trp	Arg	Asp	Val	Asn	Lys	Gly
			340					345					350		
Ser	Leu	Phe	Ile	Thr	Gln	Leu	Ile	Thr	Cys	Phe	Gln	Lys	Tyr	Ser	Trp
		355					360					365			
Cys	Phe	His	Leu	Glu	Glu	Val	Phe	Arg	Lys	Val	Gln	Gln	Ser	Phe	Glu
	370					375					380				
Lys	Pro	Asn	Val	Arg	Ala	Gln	Met	Pro	Thr	Ile	Glu	Arg	Leu	Ser	Met
385					390					395					400
Thr	Arg	Tyr	Phe	Tyr	Leu	Phe	Pro	Gly	Asn						
				405					410						

IM-5.ST25.txt

<210> 25
 <211> 1230
 <212> DNA
 <213> Felis catus

<400> 25
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 aaagcaccac gaatactttt ggaagcacgt gatgagttgt gtaatgaaga gagatccctt 180
 gttcacgtct ctccaagaca catgatgtgg ggtcgaggag cagaaagcga tgaagtcctt 240
 ctccacgtgg accttgtaaa tggcgctgct ctctagggtt tcacccacct gtgaaaggct 300
 gctacccatc tgtgaagtgc tgtccattgg ggccgctgga gagtcactga tcaacagttc 360
 ccccaaattt tcacctctgc aggcttgga gatgatgacc ttgggcttgt cctttagact 420
 aaggcagttg cgggtgttga aaatctggaa gatggtgtca taagccaata catctgggtc 480
 tccttcagcg ctgtacttcg tccacagat tccactcagg atgccatgag acatgaacac 540
 caggaatgtg ctgtccgagg acttgtgctc tggacgggca gcaaatgcc tcagctctga 600
 ttccatgtcc ttagcagtga gttcctcttt tatgtgcaca ctgtagcaa ggtctgtaag 660
 cagcctcctc atccctgcaa cgtcaaggtc agcccccttc ctgagagaaa gatgatcgaa 720
 cgctgtattg catatgatga gagccagacg agtacgatcc tttctctctt ttattgggta 780
 gatctcttca gccctctgtt tacacagttt cacgaagttt tcacgaggac aaagcttgag 840
 agcatctaca gattcttctg gctcagccgg ccagggcatg ttattcacgc tggctggaag 900
 aggaggaaac gctacttcag agtccgtggg gttctgagaa tttccagatt gtgggcttga 960
 ggagagcccc agcgtctctg caagggtgggt gtcttctctc cagatgtgac agataaagat 1020
 ctggcacgcc cgtggccctt tccgcaggac gctgtcgatc agagctcggg ccttgtccat 1080
 aacggtagcg ttttcacatt ttactctctc catctctctc tggttcagca cgtttttctc 1140
 aaagagttca tccagcaagc cgttgaccgt ccccatgccg actgagttga tgaactgctt 1200
 cctcttgccc ttcagatcct tgtcggccat 1230

<210> 26
 <211> 921
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(921)

IM-5.ST25.txt

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<400> 26
ata tgg gaa ctg gag aaa aac gtt tat gtt gta gag ttg gac tgg cac      48
Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His
1          5          10          15

cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc aat act cct gaa      96
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu
          20          25          30

gaa gat gac atc acc tgg acc tct gac cag agc agt gaa gtc cta ggc      144
Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly
          35          40          45

tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gca gat gct ggc      192
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly
          50          55          60

cag tat acc tgt cat aaa gga ggc gag gtt ctg agc cat tcg ttc ctc      240
Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu
65          70          75          80

ctg ata cac aaa aag gaa gat gga att tgg tcc act gat atc tta agg      288
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg
          85          90          95

gaa cag aaa gaa tcc aaa aat aag atc ttt cta aaa tgt gag gca aag      336
Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys
          100          105          110

aat tat tct gga cgt ttc acc tgc tgg tgg ctg acg gca atc agt acc      384
Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr
          115          120          125

gat ttg aaa ttc act gtc aaa agc agc aga ggc tcc tct gac ccc caa      432
Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
          130          135          140

gag gtg act tgt gga gca gcg aca ctc tca gca gag aag gtc aga gtg      480
Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val
145          150          155          160

gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt      528
Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
          165          170          175

gcc tgc ccg gct gcc gag gag agc cta ccc att gaa gtc gtg gtg gac      576
Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
          180          185          190

gct att cac aag ctc aag tac gaa aac tac acc agc agc ttc ttc atc      624
Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
          195          200          205

agg gac atc atc aaa ccg gac cca ccc aag aac ctg caa ctg aag cca      672
Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro
          210          215          220

tta aaa aat tct cgg cat gtg gaa gtg agc tgg gaa tac cct gac acc      720
Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr

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IM-5.ST25.txt

225		230		235		240	
tgg agc acc cca cat tcc tac ttc tcc tta aca ttt ggc gta cag gtc							768
Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val							
	245			250		255	
cag ggc aag aac aac aga gaa aag aaa gac aga ctc tcc gtg gac aag							816
Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys							
	260			265		270	
acc tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa							864
Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln							
	275			280		285	
gcc aga gac cgc tac tat agc tca tcc tgg agc aac tgg gca tcc gtg							912
Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val							
	290			295		300	
tcc tgc agt							921
Ser Cys Ser							
305							

<210> 27
 <211> 307
 <212> PRT
 <213> Felis catus

<400> 27

Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His															
1			5				10						15		
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu															
			20				25						30		
Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly															
			35				40						45		
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly															
			50				55						60		
Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu															
65						70					75				80
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg															
						85				90					95
Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys															
						100				105					110
Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr															

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115                                     120                                     125

Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
130                                     135                                     140

Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val
145                                     150                                     155                                     160

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
165                                     170                                     175

Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
180                                     185                                     190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
195                                     200                                     205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro
210                                     215                                     220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
225                                     230                                     235                                     240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val
245                                     250                                     255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys
260                                     265                                     270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
275                                     280                                     285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val
290                                     295                                     300

Ser Cys Ser
305

<210> 28
<211> 921
<212> DNA
<213> Felis catus

<400> 28
actgcaggac acggtatgcc agttgctcca ggatgagcta tagtagcggc ctctggcttg

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IM-5.ST25.txt

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cacgcggatc ttggcatcct tgtggcacac gaccttggct gaggtcttgt ccacggagag 120
tctgtctttc ttttctctgt tgttcttgcc ctggacctgt acgccaaatg ttaaggagaa 180
gtaggaatgt ggggtgctcc aggtgtcagg gtattcccag ctacttcca catgccgaga 240
atTTTTtaat ggcttcagtt gcaggttctt ggggtgggtcc ggtttgatga tgtccctgat 300
gaagaagctg ctgggtgtagt tttcgtactt gagcttgtga atagcgtcca ccacgacttc 360
aatgggtagg ctctcctcgg cagccgggca ggcactgccc tctgacact ccactgtgta 420
cttcttataa tccctgttgt ccaactctgac cttctctgct gagagtgtcg ctgctccaca 480
agtcacctct tgggggtcag aggagcctct gctgcttttg acagtgaatt tcaaatcggt 540
actgattgcc gtcagccacc agcaggtgaa acgtccagaa taattctttg cctcacattt 600
tagaaagatc ttatttttgg attctttctg ttcccttaag atatcagtgg accaaattcc 660
atcttctttt ttgtgtatca ggaggaacga atggctcaga acctcgcctc ctttatgaca 720
ggtatactgg ccagcatctg caaattcttt gacttggatg gtcagagttt taccagagcc 780
taggacttca ctgctctggg cagaggtcca ggtgatgtca tcttcttcag gagtattgca 840
ggtgaggacc accatttctc cgggggcac cagggtgccag tccaactcta caacataaac 900
gtttttctcc agttcccata t 921

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<210> 29
<211> 987
<212> DNA
<213> Felis catus

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<220>
<221> CDS
<222> (1)..(987)

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<400> 29
atg cat cct cag cag ttg gtc atc gcc tgg ttt tcc ctg gtt ttg ctg 48
Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu
1 5 10 15
gca cct ccc ctg atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt 96
Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
20 25 30
gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctg 144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45
acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag 192
Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
50 55 60
agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa 240

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IM-5.ST25.txt

Ser	Ser	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys	
65					70					75					80	
gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt																288
Glu	Phe	Ala	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val	
				85					90					95		
ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg																336
Leu	Ser	His	Ser	Phe	Leu	Leu	Ile	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp	
			100					105					110			
tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt																384
Ser	Thr	Asp	Ile	Leu	Arg	Glu	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Ile	Phe	
		115					120					125				
cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg																432
Leu	Lys	Cys	Glu	Ala	Lys	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	
	130					135					140					
ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga																480
Leu	Thr	Ala	Ile	Ser	Thr	Asp	Leu	Lys	Phe	Thr	Val	Lys	Ser	Ser	Arg	
145					150					155					160	
ggc tcc tct gac ccc caa ggg gtg act tgt gga gca gcg aca ctc tca																528
Gly	Ser	Ser	Asp	Pro	Gln	Gly	Val	Thr	Cys	Gly	Ala	Ala	Thr	Leu	Ser	
				165					170					175		
gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg																576
Ala	Glu	Lys	Val	Arg	Val	Asp	Asn	Arg	Asp	Tyr	Lys	Lys	Tyr	Thr	Val	
			180					185					190			
gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc																624
Glu	Cys	Gln	Glu	Gly	Ser	Ala	Cys	Pro	Ala	Ala	Glu	Glu	Ser	Leu	Pro	
		195				200						205				
att gaa gtc gtg gtg gac gct att cac aag ctc aag tac gaa aac tac																672
Ile	Glu	Val	Val	Val	Asp	Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	
	210					215					220					
acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag																720
Thr	Ser	Ser	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys	
225					230					235					240	
aac ctg caa ctg aag cca tta aaa aat tct cgg cat gtg gaa gtg agc																768
Asn	Leu	Gln	Leu	Lys	Pro	Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	
				245					250					255		
tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta																816
Trp	Glu	Tyr	Pro	Asp	Thr	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	
			260					265					270			
aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac																864
Thr	Phe	Gly	Val	Gln	Val	Gln	Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp	
		275					280					285				
aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat																912
Arg	Leu	Ser	Val	Asp	Lys	Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	
	290					295					300					

IM-5.ST25.txt

gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg 960
 Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
 305 310 315 320

agc aac tgg gca tcc gtg tcc tgc agt 987
 Ser Asn Trp Ala Ser Val Ser Cys Ser
 325

<210> 30
 <211> 329
 <212> PRT
 <213> Felis catus

<400> 30

Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu
 1 5 10 15

Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
 20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
 35 40 45

Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
 50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
 65 70 75 80

Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
 85 90 95

Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
 100 105 110

Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
 115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
 130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
 145 150 155 160

Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
 165 170 175

IM-5.ST25.txt

Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
260 265 270

Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
275 280 285

Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
305 310 315 320

Ser Asn Trp Ala Ser Val Ser Cys Ser
325

<210> 31
<211> 987
<212> DNA
<213> Felis catus

<400> 31
actgcaggac acggatgccc agttgctcca ggatgagcta tagtagcggc ctctggcttg 60
cacgcggatc ttggcatcct tgtggcacac gaccttggct gaggtcttgt ccacggagag 120
tctgtctttc ttttctctgt tgttcttgcc ctggacctgt acgccaaatg ttaaggagaa 180
gtaggaatgt ggggtgctcc aggtgtcagg gtattcccag ctacttcca catgccgaga 240
atTTTTTaat ggcttcagtt gcaggttctt ggggtgggtcc ggtttgatga tgtccctgat 300
gaagaagctg ctggtgtagt tttcgtactt gagcttgtga atagcgtcca ccacgacttc 360

IM-5.ST25.txt

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aatgggtagg ctctcctcgg cagccgggca ggcactgccc tcctgacact ccactgtgta 420
cttcttataa tccctgttgt ccactctgac cttctctgct gagagtgtcg ctgctccaca 480
agtcacccct tgggggtcag aggagcctct gctgcttttg acagtgaatt tcaaatcggt 540
actgattgcc gtcagccacc agcaggtgaa acgtccagaa taattctttg cctcacattt 600
tagaaagatc ttatTTTTTgg attctttctg ttcccttaag atatcagtgg accaaattcc 660
atcttctttt ttgtgtatca ggaggaacga atggctcaga acctcgctc ctttatgaca 720
gggtatactgg ccagcatctg caaattcttt gacttggatg gtcagagttt taccagagcc 780
taggacttca ctgctctggg cagaggtcca ggtgatgtca tcttcttcag gagtattgca 840
ggtgaggacc accatttctc cgggggcac accgggtgccag tccaactcta caacataaac 900
gtttttctcc agttcccata tggccatgag gggaggtgcc agcaaaacca gggaaaacca 960
ggcgatgacc aactgctgag gatgcat 987

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<210> 32
<211> 666
<212> DNA
<213> Felis catus

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<220>
<221> CDS
<222> (1)..(666)

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<400> 32
atg tgc ccg ccg cgt ggc ctc ctc ctt gta acc atc ctg gtc ctg tta 48
Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu
1 5 10 15

aac cac ctg gac cac ctc agt ttg gcc agg aac ctc ccc aca ccc aca 96
Asn His Leu Asp His Leu Ser Leu Ala Arg Asn Leu Pro Thr Pro Thr
20 25 30

cca agc cca gga atg ttc cag tgc ctc aac cac tcc caa acc ctg ctg 144
Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu
35 40 45

cga gcc atc agc aac acg ctt cag aag gcc aga caa act cta gaa ttt 192
Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe
50 55 60

tac tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aaa gat 240
Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
65 70 75 80

aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat 288
Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn
85 90 95

gag agt tgc ctg gct tcc aga gag atc tct ctg ata act aat ggg agt 336

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IM-5.ST25.txt

Glu	Ser	Cys	Leu	Ala	Ser	Arg	Glu	Ile	Ser	Leu	Ile	Thr	Asn	Gly	Ser		
			100					105					110				
tgc	ctg	gcc	tcc	aga	aag	acc	tct	ttt	atg	acg	acc	ctg	tgc	ctt	agc		384
Cys	Leu	Ala	Ser	Arg	Lys	Thr	Ser	Phe	Met	Thr	Thr	Leu	Cys	Leu	Ser		
		115					120					125					
agt	atc	tat	gag	gac	ttg	aag	atg	tac	cag	gtg	gag	ttc	aag	gcc	atg		432
Ser	Ile	Tyr	Glu	Asp	Leu	Lys	Met	Tyr	Gln	Val	Glu	Phe	Lys	Ala	Met		
	130					135					140						
aat	gca	aag	ctg	tta	atg	gat	cct	aaa	agg	cag	atc	ttt	ctg	gat	caa		480
Asn	Ala	Lys	Leu	Leu	Met	Asp	Pro	Lys	Arg	Gln	Ile	Phe	Leu	Asp	Gln		
145					150					155					160		
aac	atg	ctg	aca	gct	att	gat	gag	ctg	tta	cag	gcc	ctg	aat	gtc	aac		528
Asn	Met	Leu	Thr	Ala	Ile	Asp	Glu	Leu	Leu	Gln	Ala	Leu	Asn	Val	Asn		
				165					170					175			
agt	gtg	act	gtg	cca	cag	aac	tcc	tcc	ctg	gaa	gaa	ccg	gat	ttt	tat		576
Ser	Val	Thr	Val	Pro	Gln	Asn	Ser	Ser	Leu	Glu	Glu	Pro	Asp	Phe	Tyr		
			180					185					190				
aaa	act	aaa	atc	aag	ctc	tgc	ata	ctt	ctt	cat	gct	ttc	aga	att	cgt		624
Lys	Thr	Lys	Ile	Lys	Leu	Cys	Ile	Leu	Leu	His	Ala	Phe	Arg	Ile	Arg		
		195				200					205						
gca	gtg	acc	atc	aat	aga	atg	atg	agc	tat	ctg	aat	gct	tcc				666
Ala	Val	Thr	Ile	Asn	Arg	Met	Met	Ser	Tyr	Leu	Asn	Ala	Ser				
	210					215					220						
 <210> 33																	
<211> 222																	
<212> PRT																	
<213> Felis catus																	
 <400> 33																	
Met	Cys	Pro	Pro	Arg	Gly	Leu	Leu	Leu	Val	Thr	Ile	Leu	Val	Leu	Leu		
1				5					10					15			
Asn	His	Leu	Asp	His	Leu	Ser	Leu	Ala	Arg	Asn	Leu	Pro	Thr	Pro	Thr		
			20					25					30				
Pro	Ser	Pro	Gly	Met	Phe	Gln	Cys	Leu	Asn	His	Ser	Gln	Thr	Leu	Leu		
		35					40					45					
Arg	Ala	Ile	Ser	Asn	Thr	Leu	Gln	Lys	Ala	Arg	Gln	Thr	Leu	Glu	Phe		
	50					55					60						
Tyr	Ser	Cys	Thr	Ser	Glu	Glu	Ile	Asp	His	Glu	Asp	Ile	Thr	Lys	Asp		
65					70					75					80		

IM-5.ST25.txt

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn
85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser
100 105 110

Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser
115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met
130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn
165 170 175

Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr
180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
195 200 205

Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
210 215 220

<210> 34
<211> 666
<212> DNA
<213> Felis catus

<400> 34
ggaagcattc agatagctca tcattctatt gatggtcact gcacgaattc tgaaagcatg 60
aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggttcttcca gggaggagtt 120
ctgtggcaca gtcacactgt tgacattcag ggctgtaac agctcatcaa tagctgtcag 180
catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240
cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggctcgt 300
cataaaagag gtctttctgg aggccaggca actccatta gttatcagag agatctctct 360
ggaagccagg caactctcat tcatggttaa ttccagtggg aagcaggcct cactgtgct 420
ggttttatct tttgtgatat cttcatgac aatctcttcg gaagtgcagg agtaaaattc 480
tagagtttgt ctggccttct gaagcgtggt gctgatggct cgcagcaggg tttgggagtg 540

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gttgaggcac tgggaacattc ctgggcttgg tgtgggtgtg gggaggttcc tggccaaact      600
gaggtggtcc aggtggttta acaggaccag gatgggtaca aggaggaggc cacgcggcgg      660
gcacat                                          666

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<210> 35
<211> 591
<212> DNA
<213> Felis catus

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<220>
<221> CDS
<222> (1)..(591)

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<400> 35
agg aac ctc ccc aca ccc aca cca agc cca gga atg ttc cag tgc ctc      48
Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu
1          5          10          15

aac cac tcc caa acc ctg ctg cga gcc atc agc aac acg ctt cag aag      96
Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys
          20          25          30

gcc aga caa act cta gaa ttt tac tcc tgc act tcc gaa gag att gat      144
Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp
          35          40          45

cat gaa gat atc aca aaa gat aaa acc agc aca gtg gag gcc tgc tta      192
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
          50          55          60

cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc      240
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
65          70          75          80

tct ctg ata act aat ggg agt tgc ctg gcc tcc aga aag acc tct ttt      288
Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe
          85          90          95

atg acg acc ctg tgc ctt agc agt atc tat gag gac ttg aag atg tac      336
Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
          100          105          110

cag gtg gag ttc aag gcc atg aat gca aag ctg tta atg gat cct aaa      384
Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
          115          120          125

agg cag atc ttt ctg gat caa aac atg ctg aca gct att gat gag ctg      432
Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
          130          135          140

tta cag gcc ctg aat gtc aac agt gtg act gtg cca cag aac tcc tcc      480
Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser
145          150          155          160

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IM-5.ST25.txt

ttg gaa gaa ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt 528
 Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
 165 170 175

ctt cat gct ttc aga att cgt gca gtg acc atc aat aga atg atg agc 576
 Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
 180 185 190

tat ctg aat gct tcc 591
 Tyr Leu Asn Ala Ser
 195

<210> 36
 <211> 197
 <212> PRT
 <213> Felis catus

<400> 36

Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu
 1 5 10 15

Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys
 20 25 30

Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp
 35 40 45

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
 50 55 60

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
 65 70 75 80

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe
 85 90 95

Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
 100 105 110

Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
 115 120 125

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
 130 135 140

Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser
 145 150 155 160

IM-5.ST25.txt

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
 165 170 175

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
 180 185 190

Tyr Leu Asn Ala Ser
 195

<210> 37
 <211> 591
 <212> DNA
 <213> Felis catus

<400> 37
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 aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggttcttcca aggaggagtt 120
 ctgtggcaca gtcacactgt tgacattcag ggcctgtaac agctcatcaa tagctgtcag 180
 catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240
 cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300
 cataaaagag gtctttcttg aggccaggca actcccatta gttatcagag agatctctct 360
 ggaagccagg caactctcat tcatggttaa ttccagtggc aagcaggcct ccactgtgct 420
 ggttttatct tttgtgatat cttcatgac aatctcttcg gaagtgcagg agtaaaattc 480
 tagagtttgt ctggccttct gaagcgtggt gctgatggct cgcagcaggg tttgggagtg 540
 gttgaggcac tggaacattc ctgggcttgg tgtgggtgtg gggagggttc t 591

<210> 38
 <211> 1599
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(1599)

<400> 38
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 Met His Pro Gln Gln Leu Val Ile Ala Trp Leu Ser Leu Val Leu Leu
 1 5 10 15
 gca cct ccc ctc atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt 96
 Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
 20 25 30

IM-5.ST25.txt

gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu 35 40 45	144
acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln 50 55 60	192
agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys 65 70 75 80	240
gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val 85 90 95	288
ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp 100 105 110	336
tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe 115 120 125	384
cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp 130 135 140	432
ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg 145 150 155 160	480
ggc tcc tct gac ccc caa gag gtg act tgt gga gca gcg aca ctc tca Gly Ser Ser Asp Pro Gln Glu Val Thr Cys Gly Ala Ala Thr Leu Ser 165 170 175	528
gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val 180 185 190	576
gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro 195 200 205	624
att gaa gtc gtg gtg gac gct att cac aag ctc aag tac gaa aac tac Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr 210 215 220	672
acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys 225 230 235 240	720
aac ctg caa ctg aag cca tta aaa aat tct cgg cat gtg gaa gtg agc Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser 245 250 255	768
tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu 260 265 270	816

IM-5.ST25.txt

aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac	864
Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp	
275 280 285	
aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat	912
Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp	
290 295 300	
gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg	960
Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp	
305 310 315 320	
agc aac tgg gca tcc gtg tcc tgc agt ggt ggc ggt ggc ggc gga tct	1008
Ser Asn Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser	
325 330 335	
aga aac ttg cca acc cct act cca tcc ccg ggg atg ttc cag tgc ctc	1056
Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu	
340 345 350	
aac cac tcc caa acc ctg ctg cga gcc atc agc aac acg ctt cag aag	1104
Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys	
355 360 365	
gcc aga caa act cta gaa ttt tac tcc tgc act tcc gaa gag att gat	1152
Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp	
370 375 380	
cat gaa gat atc aca aaa gat aaa acc agc aca gtg gag gcc tgc tta	1200
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu	
385 390 395 400	
cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc	1248
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile	
405 410 415	
tct ctg ata act aat ggg agt tgc ctg gcc tcc aga aag acc tct ttt	1296
Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe	
420 425 430	
atg acg acc ctg tgc ctt agc agt atc tat gag gac ttg aag atg tac	1344
Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr	
435 440 445	
cag gtg gag ttc aag gcc atg aat gca aag ctg tta atg gat cct aaa	1392
Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys	
450 455 460	
agg cag atc ttt ctg gat caa aac atg ctg aca gct att gat gag ctg	1440
Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu	
465 470 475 480	
tta cag gcc ctg aat gtc aac agt gtg act gtg cca cag aac tcc tcc	1488
Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser	
485 490 495	
ttg gaa gaa ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt	1536
Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu	


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500                                505                                510
ctt cat gct ttc aga att cgt gca gtg acc atc aat aga atg atg agc      1584
Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
515                                520                                525

tat ctg aat gct tcc
Tyr Leu Asn Ala Ser
530                                1599

<210> 39
<211> 533
<212> PRT
<213> Felis catus

<400> 39
Met His Pro Gln Gln Leu Val Ile Ala Trp Leu Ser Leu Val Leu Leu
1                                5                                10                                15

Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
20                                25                                30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
35                                40                                45

Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
50                                55                                60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65                                70                                75                                80

Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
85                                90                                95

Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
100                                105                                110

Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
115                                120                                125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130                                135                                140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
145                                150                                155                                160

Gly Ser Ser Asp Pro Gln Glu Val Thr Cys Gly Ala Ala Thr Leu Ser

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165		170		175
Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val	180	185		190
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro	195	200		205
Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr	210	215		220
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys	225	230		240
Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser	245	250		255
Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu	260	265		270
Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp	275	280		285
Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp	290	295		300
Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp	305	310		315
Ser Asn Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser	325	330		335
Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu	340	345		350
Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys	355	360		365
Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp	370	375		380
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu	385	390		395
				400

IM-5.ST25.txt

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
405 410 415

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe
420 425 430

Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
435 440 445

Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
450 455 460

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
465 470 475 480

Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser
485 490 495

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
500 505 510

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
515 520 525

Tyr Leu Asn Ala Ser
530

<210> 40
<211> 1599
<212> DNA
<213> Felis catus

<400> 40
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aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggttcttcca aggaggagtt 120
ctgtggcaca gtcacactgt tgacattcag ggcttgtaac agtcatcaa tagctgtcag 180
catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240
cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300
cataaaagag gtctttctgg aggccaggca actccatta gttatcagag agatctctct 360
ggaagccagg caactctcat tcatggttaa ttccagtggg aagcaggcct ccactgtgct 420
ggttttatct tttgtgatat cttcatgac aatctcttcg gaagtgcagg agtaaaattc 480
tagagtttgt ctggccttct gaagcgtggt gctgatggct cgcagcaggg tttgggagtg 540

IM-5.ST25.txt

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gttgaggcac  tggaacatcc  cgggggatgg  agtaggggtt  ggcaagtttc  tagatccgcc  600
gccaccgcca  cactgcagg  acacggatgc  ccagttgctc  caggatgagc  tatagtagcg  660
gtctctgggt  tgcacggga  tcttggcatc  cttgtggcac  acgaccttgg  ctgaggctct  720
gtccacggag  agtctgtctt  tcttttctct  gttgttcttg  ccctggacct  gtacgcaaaa  780
tgttaaggag  aagtaggaat  gtggggtgct  ccaggtgtca  gggattccc  agctcacttc  840
cacatgccga  gaatttttta  atggcttcag  ttgcagggtc  ttgggtgggt  ccggtttgat  900
gatgtccctg  atgaagaagc  tgctgggtga  gttttcgtac  ttgagcttgt  gaatagcgtc  960
caccacgact  tcaatgggta  ggctctctc  ggcagccggg  caggcactgc  cctcctgaca  1020
ctccactgtg  tacttcttat  aatccctgtt  gtccactctg  accttctctg  ctgagagtgt  1080
cgctgctcca  caagtcacct  cttgggggtc  agaggagcct  ctgctgcttt  tgacagtga  1140
tttcaaatac  gtactgattg  ccgtcagcca  ccagcagggt  aaacgtccag  aataattctt  1200
tgctcacat  tttagaaga  tcttattttt  ggattctttc  tgttccctta  agatatcagt  1260
ggaccaaatt  ccattcttct  ttttgtgtat  caggaggaac  gaatggctca  gaacctcgcc  1320
tcctttatga  caggtatact  ggccagcatc  tgcaaattct  ttgacttgga  tggtcagagt  1380
tttaccagag  ctaggactt  cactgctctg  gtcagagggt  cagggtgatg  catcttcttc  1440
aggagtattg  caggtgagga  ccaccatttc  tccgggggca  tcagggtgcc  agtccaactc  1500
tacaacataa  acgtttttct  ccagttccca  tatggccatg  aggggaggtg  ccagcaaaac  1560
cagggaaagc  caggcgatga  ccaactgctg  aggatgcat  1599

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<210> 41
<211> 576
<212> DNA
<213> Felis catus

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<400> 41
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aaatgagttt  gaaaagatct  ttctcttttt  cacaagctag  aaagtacccc  ttgtacaatg  120
aagactcaaa  ttgtatctta  tcatcatgtc  ctggaacact  tctctgaaag  aatatgatgt  180
catttccttc  atcattgata  ctctcaggag  gactcatttc  cttaaaggaa  ataattttgt  240
tctcacagga  gagagtagac  atggctctat  aattcacaga  gatggttact  gccagacctc  300
tagtgagggt  atctttatac  atatatatga  taaattcagt  ccgggggtgca  ttatctgtac  360
agtcagaatc  aggcataatc  tcaaacacag  gttgatctcc  ctgggttaatg  aagagaactt  420
ggtcgttcaa  gtttcgtaag  attgagagtt  tatgttcaag  cttgccaaag  taatctgttt  480

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ccagggttttc atcactgtca gctacaaagt aaagtgtatt gtcaataaat ttcattccca 540
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<210> 42
 <211> 0
 <212> DNA
 <213> Felis catus

<400> 42
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<210> 43
 <211> 1533
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(1533)

<400> 43
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 Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His
 1 5 10 15
 cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc aat act cct gaa 96
 Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu
 20 25 30
 gaa gat gac atc acc tgg acc tct gac cag agc agt gaa gtc cta ggc 144
 Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly
 35 40 45
 tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gca gat gct ggc 192
 Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly
 50 55 60
 cag tat acc tgt cat aaa gga ggc gag gtt ctg agc cat tcg ttc ctc 240
 Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu
 65 70 75 80
 ctg ata cac aaa aag gaa gat gga att tgg tcc act gat atc tta agg 288
 Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg
 85 90 95
 gaa cag aaa gaa tcc aaa aat aag atc ttt cta aaa tgt gag gca aag 336
 Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys
 100 105 110
 aat tat tct gga cgt ttc acc tgc tgg tgg ctg acg gca atc agt acc 384
 Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr
 115 120 125
 gat ttg aaa ttc act gtc aaa agc agc aga ggc tcc tct gac ccc caa 432
 Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln

IM-5.ST25.txt

130	135	140	
gag gtg act tgt gga gca gcg aca ctc tca gca gag aag gtc aga gtg Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val 145 150 155 160			480
gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser 165 170 175			528
gcc tgc ccg gct gcc gag gag agc cta ccc att gaa gtc gtg gtg gac Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp 180 185 190			576
gct att cac aag ctc aag tac gaa aac tac acc agc agc ttc ttc atc Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile 195 200 205			624
agg gac atc atc aaa ccg gac cca ccc aag aac ctg caa ctg aag cca Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro 210 215 220			672
tta aaa aat tct cgg cat gtg gaa gtg agc tgg gaa tac cct gac acc Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr 225 230 235 240			720
tgg agc acc cca cat tcc tac ttc tcc tta aca ttt ggc gta cag gtc Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val 245 250 255			768
cag ggc aag aac aac aga gaa aag aaa gac aga ctc tcc gtg gac aag Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys 260 265 270			816
acc tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln 275 280 285			864
gcc aga gac cgc tac tat agc tca tcc tgg agc aac tgg gca tcc gtg Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val 290 295 300			912
tcc tgc agt ggt ggc ggt ggc ggc gga tct aga aac ttg cca acc cct Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser Arg Asn Leu Pro Thr Pro 305 310 315 320			960
act cca tcc ccg ggg atg ttc cag tgc ctc aac cac tcc caa acc ctg Thr Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu 325 330 335			1008
ctg cga gcc atc agc aac acg ctt cag aag gcc aga caa act cta gaa Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu 340 345 350			1056
ttt tac tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aaa Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys 355 360 365			1104
gat aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg			1152

IM-5.ST25.txt

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Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met
370                               375                               380

aat gag agt tgc ctg gct tcc aga gag atc tct ctg ata act aat ggg      1200
Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly
385                               390                               395                               400

agt tgc ctg gcc tcc aga aag acc tct ttt atg acg acc ctg tgc ctt      1248
Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu
                               405                               410                               415

agc agt atc tat gag gac ttg aag atg tac cag gtg gag ttc aag gcc      1296
Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala
                               420                               425                               430

atg aat gca aag ctg tta atg gat cct aaa agg cag atc ttt ctg gat      1344
Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp
                               435                               440                               445

caa aac atg ctg aca gct att gat gag ctg tta cag gcc ctg aat gtc      1392
Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val
                               450                               455                               460

aac agt gtg act gtg cca cag aac tcc tcc ttg gaa gaa ccg gat ttt      1440
Asn Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe
465                               470                               475                               480

tat aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att      1488
Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile
                               485                               490                               495

cgt gca gtg acc atc aat aga atg atg agc tat ctg aat gct tcc      1533
Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
                               500                               505                               510

<210> 44
<211> 511
<212> PRT
<213> Felis catus

<400> 44

Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His
1                               5                               10                               15

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu
20                               25                               30

Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly
35                               40                               45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly
50                               55                               60

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IM-5.ST25.txt

Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu
 65 70 75 80

Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg
 85 90 95

Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys
 100 105 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr
 115 120 125

Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
 130 135 140

Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val
 145 150 155 160

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
 165 170 175

Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
 180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
 195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro
 210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
 225 230 235 240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val
 245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys
 260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
 275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val
 290 295 300

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Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser Arg Asn Leu Pro Thr Pro
305 310 315 320

Thr Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu
325 330 335

Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu
340 345 350

Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys
355 360 365

Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met
370 375 380

Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly
385 390 395 400

Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu
405 410 415

Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala
420 425 430

Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp
435 440 445

Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val
450 455 460

Asn Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe
465 470 475 480

Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile
485 490 495

Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
500 505 510

<210> 45

<211> 1533

<212> DNA

<213> Felis catus

<400> 45

IM-5.ST25.txt

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aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggttcttcca aggaggagt	120
ctgtggcaca gtcacactgt tgacattcag ggcctgtaac agctcatcaa tagctgtcag	180
catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc	240
cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggctcg	300
cataaaagag gtctttcttg aggccaggca actcccatta gttatcagag agatctctct	360
ggaagccagg caactctcat tcatgggtaa ttccagtggg aagcaggcct ccaactgtgct	420
ggttttatct tttgtgatat cttcatgac aatctcttcg gaagtgcagg agtaaaattc	480
tagagtttgt ctggccttct gaagcgtggt gctgatggct cgcagcaggg tttgggagt	540
gttgaggcac tggaacatcc ccggggatgg agtaggggtt ggcaagtttc tagatccgcc	600
gccaccgcca ccaactgcagg acacggatgc ccagttgctc caggatgagc tatagtagcg	660
gtctctggct tgcacgcgga tcttggcatc cttgtggcac acgaccttgg ctgaggctct	720
gtccacggag agtctgtctt tcttttctct gttgttcttg ccctggacct gtacgcaaaa	780
tgtaaggag aagtaggaat gtgggggtgct ccagggtgtca gggattccc agctcacttc	840
cacatgccga gaatttttta atggcttcag ttgcagggtc ttgggtgggt ccggtttgat	900
gatgtccctg atgaagaagc tgctgggtga gttttcgtac ttgagcttgt gaatagcgtc	960
caccacgact tcaatgggta ggctctctc gccagccggg caggcactgc cctcctgaca	1020
ctccactgtg tacttcttat aatccctgtt gtccactctg accttctctg ctgagagtgt	1080
cgctgtcca caagtcacct cttgggggtc agaggagcct ctgctgcttt tgacagtga	1140
tttcaaactg gtactgattg ccgtcagcca ccagcagggtg aaacgtccag aataattctt	1200
tgccctacat tttagaaaga tcttattttt ggattctttc tgttccctta agatatcagt	1260
ggaccaaatt ccatcttctt ttttgtgtat caggaggaac gaatggctca gaacctcgcc	1320
tcctttatga caggataact ggccagcatc tgcaaattct ttgacttga tggtcagagt	1380
tttaccagag cctaggactt cactgctctg gtcagagggtc cagggtgatgt catcttcttc	1440
aggagtattg caggtgagga ccaccatttc tccgggggca tcagggtgcc agtccaactc	1500
tacaacataa acgtttttct ccagttccca tat	1533

<210> 46
 <211> 666
 <212> DNA
 <213> Canis familiaris

<220>

<221> CDS

<222> (1)..(666)

<400> 46

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Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu	
1 5 10 15	
agc cac ctg gac cac ctt act tgg gcc agg agc ctc ccc aca gcc tca	96
Ser His Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser	
20 25 30	
ccg agc cca gga ata ttc cag tgc ctc aac cac tcc caa aac ctg ctg	144
Pro Ser Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu	
35 40 45	
aga gcc gtc agc aac acg ctt cag aag gcc aga caa act cta gaa tta	192
Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu	
50 55 60	
tat tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aag gat	240
Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp	
65 70 75 80	
aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat	288
Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn	
85 90 95	
gag agt tgc ctg gct tcc aga gag atc tct ttg ata act aac ggg agt	336
Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser	
100 105 110	
tgc ctg gcc tct gga aag gcc tct ttt atg acg gtc ctg tgc ctt agc	384
Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser	
115 120 125	
agc atc tat gag gac ttg aag atg tac cag atg gaa ttc aag gcc atg	432
Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met	
130 135 140	
aac gca aag ctt tta atg gat ccc aag agg cag atc ttt ctg gat caa	480
Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln	
145 150 155 160	
aac atg ctg aca gct atc gat gag ctg tta cag gcc ctg aat ttc aac	528
Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn	
165 170 175	
agt gtg act gtg cca cag aaa tcc tcc ctt gaa gag ccg gat ttt tat	576
Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr	
180 185 190	
aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt	624
Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg	
195 200 205	
gcg gtg acc atc gat aga atg atg agt tat ctg aat tct tcc	666
Ala Val Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser	

210

215

220

<210> 47
 <211> 222
 <212> PRT
 <213> Canis familiaris

<400> 47

Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu
 1 5 10 15

Ser His Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser
 20 25 30

Pro Ser Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu
 35 40 45

Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu
 50 55 60

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
 65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn
 85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser
 100 105 110

Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser
 115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met
 130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
 145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn
 165 170 175

Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr
 180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg

195

200

205

Ala Val Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser
 210 215 220

<210> 48
 <211> 666
 <212> DNA
 <213> Canis familiaris

<400> 48
 ggaagaattc agataactca tcattctatc gatggtcacc gcacgaattc tgaaagcatg 60
 aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggctcttcaa gggaggattt 120
 ctgtggcaca gtcacactgt tgaaattcag ggctgtaac agctcatcga tagctgtcag 180
 catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240
 cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt 300
 cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct 360
 ggaagccagg caactctcat tcatggttaa ttccagtggg aagcaggcct ccactgtgct 420
 ggttttatcc tttgtgatat ctcatgatc aatctcttcg gaagtgcagg aatataattc 480
 tagagtttgt ctggccttct gaagcgtggt gctgacggct ctcagcaggt tttgggagtg 540
 gttgaggcac tggaatatcc ctgggctcgg tgaggctgtg gggaggctcc tggcccaagt 600
 aaggtggtcc aggtggctta gcaggaccag gatggtcaca aggaggaggc cgcgcggcgg 660
 gcacat 666

<210> 49
 <211> 591
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (1)..(591)

<400> 49
 agg agc ctc ccc aca gcc tca ccg agc cca gga ata ttc cag tgc ctc 48
 Arg Ser Leu Pro Thr Ala Ser Pro Ser Pro Gly Ile Phe Gln Cys Leu
 1 5 10 15
 aac cac tcc caa aac ctg ctg aga gcc gtc agc aac acg ctt cag aag 96
 Asn His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys
 20 25 30
 gcc aga caa act cta gaa tta tat tcc tgc act tcc gaa gag att gat 144
 Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp

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35	40	45	
cat gaa gat atc aca aag gat aaa acc agc aca gtg gag gcc tgc tta			192
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu			
50	55	60	
cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc			240
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile			
65	70	75	80
tct ttg ata act aac ggg agt tgc ctg gcc tct gga aag gcc tct ttt			288
Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe			
	85	90	95
atg acg gtc ctg tgc ctt agc agc atc tat gag gac ttg aag atg tac			336
Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr			
	100	105	110
cag atg gaa ttc aag gcc atg aac gca aag ctt tta atg gat ccc aag			384
Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys			
	115	120	125
agg cag atc ttt ctg gat caa aac atg ctg aca gct atc gat gag ctg			432
Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu			
	130	135	140
tta cag gcc ctg aat ttc aac agt gtg act gtg cca cag aaa tcc tcc			480
Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser			
	145	150	155
ctt gaa gag ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt			528
Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu			
	165	170	175
ctt cat gct ttc aga att cgt gcg gtg acc atc gat aga atg atg agt			576
Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Met Met Ser			
	180	185	190
tat ctg aat tct tcc			591
Tyr Leu Asn Ser Ser			
	195		

<210> 50
 <211> 197
 <212> PRT
 <213> Canis familiaris

<400> 50

Arg Ser Leu Pro Thr Ala Ser Pro Ser Pro Gly Ile Phe Gln Cys Leu
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Asn His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys
20 25 30

Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp

35

40

45

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
 50 55 60

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
 65 70 75 80

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe
 85 90 95

Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
 100 105 110

Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
 115 120 125

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
 130 135 140

Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser
 145 150 155 160

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
 165 170 175

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Met Met Ser
 180 185 190

Tyr Leu Asn Ser Ser
 195

<210> 51
 <211> 591
 <212> DNA
 <213> Canis familiaris

<400> 51
 ggaagaattc agataactca tcattctatc gatggtcacc gcacgaattc tgaaagcatg 60
 aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggctcttcaa gggaggattt 120
 ctgtggcaca gtcacactgt tgaaattcag ggctgtaac agctcatcga tagctgtcag 180
 catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240
 cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt 300

IM-5.ST25.txt

cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct	360
ggaagccagg caactctcat tcatgggttaa ttccagtggg aagcaggcct ccactgtgct	420
ggtttttatcc tttgtgatat cttcatgata aatctcttcg gaagtgcagg aatataattc	480
tagagtttgt ctggccttct gaagcgtggt gctgacggct ctcagcaggt tttgggagtg	540
gttgaggcac tggaatatcc ctgggctcgg tgaggctgtg gggaggctcc t	591

<210> 52
 <211> 921
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (1)..(921)

<400> 52	
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Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His	
1 5 10 15	
cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc cat acc cct gaa	96
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu	
20 25 30	
gaa gat gac atc act tgg acc tca gcg cag agc agt gaa gtc cta ggt	144
Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly	
35 40 45	
tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gga gat gct ggc	192
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly	
50 55 60	
cag tat acc tgc cat aaa gga ggc aag gtt ctg agc cgc tca ctc ctg	240
Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu	
65 70 75 80	
ttg att cac aaa aaa gaa gat gga att tgg tcc act gat atc tta aag	288
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys	
85 90 95	
gaa cag aaa gaa tcc aaa aat aag atc ttt ctg aaa tgt gag gca aag	336
Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys	
100 105 110	
aat tat tct gga cgt ttc aca tgc tgg tgg ctg acg gca atc agt act	384
Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr	
115 120 125	
gat ttg aaa ttc agt gtc aaa agt agc aga ggc ttc tct gac ccc caa	432
Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln	
130 135 140	
ggg gtg aca tgt gga gca gtg aca ctt tca gca gag agg gtc aga gtg	480

IM-5.ST25.txt

Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val	
145 150 155 160	
gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt	528
Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser	
165 170 175	
gcc tgc ccc tct gcc gag gag agc cta ccc atc gag gtc gtg gtg gat	576
Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp	
180 185 190	
gct att cac aag ctc aag tat gaa aac tac acc agc agc ttc ttc atc	624
Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile	
195 200 205	
aga gac atc atc aaa cca gac cca ccc aca aac ctg cag ctg aag cca	672
Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro	
210 215 220	
ttg aaa aat tct cgg cac gtg gag gtc agc tgg gaa tac ccc gac acc	720
Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr	
225 230 235 240	
tgg agc acc cca cat tcc tac ttc tcc ctg aca ttt tgc ata cag gcc	768
Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala	
245 250 255	
cag ggc aag aac aat aga gaa aag aaa gat aga ctc tgc gtg gac aag	816
Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys	
260 265 270	
acc tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa	864
Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln	
275 280 285	
gcc cga gac cgc tac tat agt tca tcc tgg agc gac tgg gca tct gtg	912
Ala Arg Asp Arg Tyr Tyr Ser Ser Trp Ser Asp Trp Ala Ser Val	
290 295 300	
tcc tgc agt	921
Ser Cys Ser	
305	
<210> 53	
<211> 307	
<212> PRT	
<213> Canis familiaris	
<400> 53	
Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His	
1 5 10 15	
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu	
20 25 30	

IM-5.ST25.txt

Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly
 35 40 45
 Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
 50 55 60
 Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu
 65 70 75 80
 Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
 85 90 95
 Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys
 100 105 110
 Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr
 115 120 125
 Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln
 130 135 140
 Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val
 145 150 155 160
 Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
 165 170 175
 Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
 180 185 190
 Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
 195 200 205
 Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro
 210 215 220
 Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
 225 230 235 240
 Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala
 245 250 255
 Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys
 260 265 270

IM-5.ST25.txt

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
 275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val
 290 295 300

Ser Cys Ser
 305

<210> 54
 <211> 921
 <212> DNA
 <213> Canis familiaris

<400> 54
 actgcaggac acagatgccc agtcgctcca ggatgaacta tagtagcggg ctcgggcttg 60
 cacgcggtac ttggcatcct tgtggcacac gaccttggct gaggtcttgt ccacgcagag 120
 tctatctttc ttttctctat tgttcttgcc ctgggcctgt atgcaaaatg tcagggagaa 180
 gtaggaatgt ggggtgctcc aggtgtcggg gtattcccag ctgacctcca cgtgccgaga 240
 atttttcaat ggcttcagct gcaggtttgt ggggtgggtct ggtttgatga tgtctctgat 300
 gaagaagctg ctggtgtagt tttcatactt gagcttgtga atagcatcca ccacgacctc 360
 gatgggtagg ctctcctcgg cagaggggca ggcactgccc tcctgacact ccactgtgta 420
 cttcttataa tcctgttgt ccactctgac cctctctgct gaaagtgtca ctgctccaca 480
 tgtcaccctt tgggggtcag agaagcctct gctacttttg aactgaatt tcaaatcagt 540
 actgattgcc gtcagccacc agcatgtgaa acgtccagaa taattctttg cctcacattt 600
 cagaaagatc ttatttttgg attctttctg ttcctttaag atatcagtgg accaaattcc 660
 atcttctttt ttgtgaatca acaggagtga gcggtcaga accttgctc ctttatggca 720
 ggtatactgg ccagcatctc caaattcttt gacttggatg gtcagagttt taccagaacc 780
 taggacttca ctgctctgcg ctgaggtcca agtgatgtca tcttcttcag gggtatggca 840
 ggtgaggacc accatttctc cgggggcatc agggtgccag tccaactcta caacataaac 900
 atctttctcc agttcccata t 921

<210> 55
 <211> 985
 <212> DNA
 <213> Felis catus

<220>

<221> CDS

<222> (1)..(984)

<400> 55

atg cat cct cag cag ttg gtc atc gcc tgg ttt tcc ctg gtt ttg ctg	48
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1 5 10 15	
gca cct ccc ctc atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt	96
Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val	
20 25 30	
gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc	144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu	
35 40 45	
acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag	192
Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln	
50 55 60	
agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa	240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys	
65 70 75 80	
gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt	288
Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val	
85 90 95	
ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg	336
Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp	
100 105 110	
tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt	384
Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe	
115 120 125	
cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg	432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp	
130 135 140	
ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga	480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg	
145 150 155 160	
ggc tcc tct gac ccc caa ggg gtg act tgt gga gca gcg aca ctc tca	528
Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser	
165 170 175	
gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg	576
Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val	
180 185 190	
gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc	624
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro	
195 200 205	
att gaa gtc gtg gtg gac gct att cac aag ctc aag tac gaa aac tac	672
Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr	
210 215 220	

IM-5.ST25.txt

acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag 720
 Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
 225 230 235 240

aac ctg caa ctg aag cca tta aaa aat tct cgg cat gtg gaa gtg agc 768
 Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
 245 250 255

tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta 816
 Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
 260 265 270

aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac 864
 Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
 275 280 285

aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat 912
 Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
 290 295 300

gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg 960
 Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
 305 310 315 320

agc aac tgg gca tcc gtg tcc tgc a 985
 Ser Asn Trp Ala Ser Val Ser Cys
 325

<210> 56

<211> 328

<212> PRT

<213> Felis catus

<400> 56

Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu
 1 5 10 15

Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
 20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
 35 40 45

Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
 50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
 65 70 75 80

Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
 85 90 95

IM-5.ST25.txt

Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
 100 105 110
 Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
 115 120 125
 Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
 130 135 140
 Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
 145 150 155 160
 Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
 165 170 175
 Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
 180 185 190
 Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
 195 200 205
 Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
 210 215 220
 Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
 225 230 235 240
 Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
 245 250 255
 Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
 260 265 270
 Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
 275 280 285
 Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
 290 295 300
 Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
 305 310 315 320
 Ser Asn Trp Ala Ser Val Ser Cys

325

<210> 57
 <211> 985
 <212> DNA
 <213> Felis catus

<400> 57
 tgcaggacac ggatgccagc ttgctccagg atgagctata gtagcggctc ctggccttgca 60
 cgcggatcct ggcatccttg tggcacacga ccttggtgta ggtcttggtc acggagagtc 120
 tgtctttctt ttctctgttg ttcttgccct ggacctgtac gccaaatgtt aaggagaagt 180
 aggaatgtgg ggtgctccag gtgtcagggc attcccagct cacttccaca tgccgagaat 240
 tttttaatgg cttcagttgc aggttcttgg gtgggtccgg tttgatgatg tccctgatga 300
 agaagctgct ggtgtagttt tcgtacttga gcttgatgaat agcgtccacc acgacttcaa 360
 tgggtaggct ctctcgggca gccgggcagg cactgccctc ctgacactcc actgtgtact 420
 tcttataatc cctgttggtc actctgacct tctctgctga gagtgtcgtc gctccacaag 480
 tcaccccttg ggggtcagag gagcctctgc tgcttttgac agtgaatttc aaatcgggtac 540
 tgattgccgt cagccaccag caggtgaaac gtccagaata attctttgcc tcacatttta 600
 gaaagatcct atttttggat tctttctgtt cccttaagat atcagtggac caaattccat 660
 cttccttttt gtgtatcagg aggaacgaat ggctcagaac ctgcctcctt ttatgacagg 720
 tatactggcc agcatctgca aattctttga cttggatggc cagagtttta ccagagccta 780
 ggacttcact gctctgggtc gaggtccagg tgatgtcatc ttcttcagga gtattgcagg 840
 tgaggaccac catttctccg ggggcatcag ggtgccagtc caactctaca acataaacgt 900
 ttttctccag ttcccatatg gccatgaggg gaggtgccag caaaaccagg gaaaaccagg 960
 cgatgaccaa ctgctgagga tgcac 985

<210> 58
 <211> 987
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (1)..(987)

<400> 58
 atg cac cct cag cag ttg gtc atc tcc tgg ttt tcc ctg gtt ttg ctg 48
 Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu
 1 5 10 15

IM-5.ST25.txt

gcg tct ccc ctc atg gcc ata tgg gaa ctg gag aaa gat gtt tat gtt	96
Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val	
20 25 30	
gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc	144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu	
35 40 45	
acc tgc cat acc cct gaa gaa gat gac atc act tgg acc tca gcg cag	192
Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln	
50 55 60	
agc agt gaa gtc cta ggt tct ggt aaa act ctg acc atc caa gtc aaa	240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys	
65 70 75 80	
gaa ttt gga gat gct ggc cag tat acc tgc cat aaa gga ggc aag gtt	288
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val	
85 90 95	
ctg agc cgc tca ctc ctg ttg att cac aaa aaa gaa gat gga att tgg	336
Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp	
100 105 110	
tcc act gat atc tta aag gaa cag aaa gaa tcc aaa aat aag atc ttt	384
Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe	
115 120 125	
ctg aaa tgt gag gca aag aat tat tct gga cgt ttc aca tgc tgg tgg	432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp	
130 135 140	
ctg acg gca atc agt act gat ttg aaa ttc agt gtc aaa agt agc aga	480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg	
145 150 155 160	
ggc ttc tct gac ccc caa ggg gtg aca tgt gga gca gtg aca ctt tca	528
Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser	
165 170 175	
gca gag agg gtc aga gtg gac aac agg gat tat aag aag tac aca gtg	576
Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val	
180 185 190	
gag tgt cag gag ggc agt gcc tgc ccc tct gcc gag gag agc cta ccc	624
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro	
195 200 205	
atc gag gtc gtg gtg gat gct att cac aag ctc aag tat gaa aac tac	672
Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr	
210 215 220	
acc agc agc ttc ttc atc aga gac atc atc aaa cca gac cca ccc aca	720
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr	
225 230 235 240	
aac ctg cag ctg aag cca ttg aaa aat tct cgg cac gtg gag gtc agc	768
Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser	
245 250 255	

IM-5.ST25.txt

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tgg gaa tac ccc gac acc tgg agc acc cca cat tcc tac ttc tcc ctg      816
Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
      260                      265                      270

aca ttt tgc ata cag gcc cag ggc aag aac aat aga gaa aag aaa gat      864
Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
      275                      280                      285

aga ctc tgc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat      912
Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
      290                      295                      300

gcc aag atc cgc gtg caa gcc cga gac cgc tac tat agt tca tcc tgg      960
Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
      305                      310                      315                      320

agc gac tgg gca tct gtg tca tgc agt
Ser Asp Trp Ala Ser Val Ser Cys Ser      987
      325

```

```

<210> 59
<211> 329
<212> PRT
<213> Canis familiaris

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<400> 59

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Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu
1          5          10          15

Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val
      20          25          30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
      35          40          45

Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln
      50          55          60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65          70          75          80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val
      85          90          95

Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
      100         105         110

Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
      115         120         125

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IM-5.ST25.txt

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
 130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg
 145 150 155 160

Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser
 165 170 175

Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
 180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro
 195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
 210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr
 225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
 245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
 260 265 270

Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
 275 280 285

Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
 290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
 305 310 315 320

Ser Asp Trp Ala Ser Val Ser Cys Ser
 325

<210> 60
 <211> 987
 <212> DNA
 <213> Canis familiaris

IM-5.ST25.txt

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<400> 60
actgcatgac acagatgccc agtcgctcca ggatgaacta tagtagcggt ctcgggcttg      60
cacgcggatc ttggcatcct tgtggcacac gaccttggt gaggtcttgt ccacgcagag      120
tctatctttc ttttctctat tgttcttgcc ctgggcctgt atgcaaaatg tcagggagaa      180
gtaggaatgt ggggtgctcc aggtgtcggg gtattcccag ctgacctcca cgtgccgaga      240
atttttcaat ggcttcagct gcaggtttgt ggggtgggtct ggtttgatga tgtctctgat      300
gaagaagctg ctggtgtagt tttcatactt gagcttgtga atagcatcca ccacgacctc      360
gatgggtagg ctctcctcgg cagaggggca ggcactgccc tctgacact ccactgtgta      420
cttcttataa tccctgttgt ccactctgac cctctctgct gaaagtgtca ctgctccaca      480
tgtcaccctt tgggggtcag agaagcctct gctacttttg aactgaatt tcaaatacagt      540
actgattgcc gtcagccacc agcatgtgaa acgtccagaa taattctttg cctcacattt      600
cagaaagatc ttatTTTTTg attctttctg ttcctttaag atatcagtgg accaaattcc      660
atcttctttt ttgtgaatca acaggagtga gcggtcaga accttgacct ctttatggca      720
ggtatactgg ccagcatctc caaattcttt gacttgatg gtcagagttt taccagaacc      780
taggacttca ctgctctgcg ctgaggcca agtgatgtca tcttcttcag gggtatggca      840
ggtgaggacc accatttctc cgggggcac agggtgccag tccaactcta caacataaac      900
atctttctcc agttccata tggccatgag gggagacgcc agcaaacga gggaaaacca      960
ggagatgacc aactgctgag ggtgcat                                         987

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<210> 61
<211> 1599
<212> DNA
<213> Canis familiaris

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<220>
<221> CDS
<222> (1)..(1599)

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<400> 61
atg cac cct cag cag ttg gtc atc tcc tgg ttt tcc ctc gtt ttg ctg      48
Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu
1          5          10          15

gcg tct ccc ctc atg gcc ata tgg gaa ctg gag aaa gat gtt tat gtt      96
Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val
20          25          30

gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc      144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
35          40          45

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IM-5.ST25.txt

acc tgc cat acc cct gaa gaa gat gac atc act tgg acc tca gcg cag	192
Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln	
50 55 60	
agc agt gaa gtc cta ggt tct ggt aaa act ctg acc atc caa gtc aaa	240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys	
65 70 75 80	
gaa ttt gga gat gct ggc cag tat acc tgc cat aaa gga ggc aag gtt	288
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val	
85 90 95	
ctg agc cgc tca ctc ctg ttg att cac aaa aaa gaa gat gga att tgg	336
Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp	
100 105 110	
tcc act gat atc tta aag gaa cag aaa gaa tcc aaa aat aag atc ttt	384
Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe	
115 120 125	
ctg aaa tgt gag gca aag aat tat tct gga cgt ttc aca tgc tgg tgg	432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp	
130 135 140	
ctg acg gca atc agt act gat ttg aaa ttc agt gtc aaa agt agc aga	480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg	
145 150 155 160	
ggc ttc tct gac ccc caa ggg gtg aca tgt gga gca gtg aca ctt tca	528
Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser	
165 170 175	
gca gag agg gtc aga gtg gac aac agg gat tat aag aag tac aca gtg	576
Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val	
180 185 190	
gag tgt cag gag ggc agt gcc tgc ccc tct gcc gag gag agc cta ccc	624
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro	
195 200 205	
atc gag gtc gtg gtg gat gct att cac aag ctc aag tat gaa aac tac	672
Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr	
210 215 220	
acc agc agc ttc ttc atc aga gac atc atc aaa cca gac cca ccc aca	720
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr	
225 230 235 240	
aac ctg cag ctg aag cca ttg aaa aat tct cgg cac gtg gag gtc agc	768
Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser	
245 250 255	
tgg gaa tac ccc gac acc tgg agc acc cca cat tcc tac ttc tcc ctg	816
Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu	
260 265 270	
aca ttt tgc ata cag gcc cag ggc aag aac aat aga gaa aag aaa gat	864
Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp	
275 280 285	

IM-5.ST25.txt

aga ctc tgc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat	912
Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp	
290 295 300	
gcc aag atc cgc gtg caa gcc cga gac cgc tac tat agt tca tcc tgg	960
Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp	
305 310 315 320	
agc gac tgg gca tct gtg tca tgc agt ggt ggc ggt ggc ggc gga tct	1008
Ser Asp Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser	
325 330 335	
aga aac ttg cca acc cct act cca tcc ccg ggt atg ttc caa tgt ttg	1056
Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu	
340 345 350	
aac cac tcc caa acc ttg ttg aga gcc gtc agc aac acg ctt cag aag	1104
Asn His Ser Gln Thr Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys	
355 360 365	
gcc aga caa act cta gaa tta tat tcc tgc act tcc gaa gag att gat	1152
Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp	
370 375 380	
cat gaa gat atc aca aag gat aaa acc agc aca gtg gag gcc tgc tta	1200
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu	
385 390 395 400	
cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc	1248
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile	
405 410 415	
tct ttg ata act aac ggg agt tgc ctg gcc tct gga aag gcc tct ttt	1296
Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe	
420 425 430	
atg acg gtc ctg tgc ctt agc agc atc tat gag gac ttg aag atg tac	1344
Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr	
435 440 445	
cag atg gaa ttc aag gcc atg aac gca aag ctt tta atg gat ccc aag	1392
Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys	
450 455 460	
agg cag atc ttt ctg gat caa aac atg ctg aca gct atc gat gag ctg	1440
Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu	
465 470 475 480	
tta cag gcc ctg aat ttc aac agt gtg act gtg cca cag aaa tcc tcc	1488
Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser	
485 490 495	
ctt gaa gag ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt	1536
Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu	
500 505 510	
ctt cat gct ttc aga att cgt gcg gtg acc atc aat aga atg atg tcc	1584
Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser	

515

520

525

tac ttg aac tct tcc
 Tyr Leu Asn Ser Ser
 530

1599

<210> 62
 <211> 533
 <212> PRT
 <213> Canis familiaris
 <400> 62

Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu
 1 5 10 15

Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val
 20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
 35 40 45

Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln
 50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
 65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val
 85 90 95

Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
 100 105 110

Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
 115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
 130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg
 145 150 155 160

Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser
 165 170 175

Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val

180		185		190
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro	195	200	205	
Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr	210	215	220	
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr	225	230	235	240
Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser	245	250	255	
Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu	260	265	270	
Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp	275	280	285	
Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp	290	295	300	
Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp	305	310	315	320
Ser Asp Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser	325	330	335	
Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu	340	345	350	
Asn His Ser Gln Thr Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys	355	360	365	
Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp	370	375	380	
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu	385	390	395	400
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile	405	410	415	

IM-5.ST25.txt

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe
420 425 430

Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
435 440 445

Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
450 455 460

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
465 470 475 480

Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser
485 490 495

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
500 505 510

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
515 520 525

Tyr Leu Asn Ser Ser
530

<210> 63
<211> 1599
<212> DNA
<213> Canis familiaris

<400> 63
ggaagagttc aagtaggaca tcattctatt gatggtcacc gcacgaattc tgaaagcatg 60
aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggctcttcaa gggaggattt 120
ctgtggcaca gtcacactgt tgaaattcag ggcttgtaac agctcatcga tagctgtcag 180
catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240
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cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct 360
ggaagccagg caactctcat tcatggttaa ttccagtggg aagcaggcct ccactgtgct 420
ggtttttatcc tttgtgatat cttcatgatc aatctcttcg gaagtgcagg aatataattc 480
tagagtttgt ctggccttct gaagcgtggt gctgacggct ctcaacaagg tttgggagtg 540
gttcaaacat tggaacatac ccgggggatgg agtaggggtt ggcaagtttc tagatccgcc 600
gccaccgcca ccactgcatg acacagatgc ccagtcgctc caggatgaac tatagtagcg 660

IM-5.ST25.txt

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gtctcggggt tgcacgcgga tcttggcatt cttgtggcac acgaccttgg ctgaggtctt 720
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tgtcagggag aagtaggaat gtgggggtgt ccaggtgtcg gggatttccc agctgacctc 840
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gatgtctctg atgaagaagc tgctgggtga gttttcatac ttgagcttgt gaatagcatc 960
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tacaacataa acatctttct ccagttccca tatggccatg aggggagacg ccagcaaaac 1560
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<210> 64
<211> 0
<212> DNA
<213> Canis familiaris

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<400> 64
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<210> 65
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<400> 65
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```

<210> 66
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<212> DNA
<213> Canis familiaris

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<220>
<221> CDS
<222> (1)..(1533)

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IM-5.ST25.txt

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Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His
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cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc cat acc cct gaa      96
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu
      20      25      30

gaa gat gac atc act tgg acc tca gcg cag agc agt gaa gtc cta ggt      144
Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly
      35      40      45

tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gga gat gct ggc      192
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
      50      55      60

cag tat acc tgc cat aaa gga ggc aag gtt ctg agc cgc tca ctc ctg      240
Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu
65      70      75      80

ttg att cac aaa aaa gaa gat gga att tgg tcc act gat atc tta aag      288
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
      85      90      95

gaa cag aaa gaa tcc aaa aat aag atc ttt ctg aaa tgt gag gca aag      336
Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys
      100      105      110

aat tat tct gga cgt ttc aca tgc tgg tgg ctg acg gca atc agt act      384
Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr
      115      120      125

gat ttg aaa ttc agt gtc aaa agt agc aga ggc ttc tct gac ccc caa      432
Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln
      130      135      140

ggg gtg aca tgt gga gca gtg aca ctt tca gca gag agg gtc aga gtg      480
Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val
      145      150      155      160

gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt      528
Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
      165      170      175

gcc tgc ccc tct gcc gag gag agc cta ccc atc gag gtc gtg gtg gat      576
Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
      180      185      190

gct att cac aag ctc aag tat gaa aac tac acc agc agc ttc ttc atc      624
Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
      195      200      205

aga gac atc atc aaa cca gac cca ccc aca aac ctg cag ctg aag cca      672
Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro
      210      215      220

ttg aaa aat tct cgg cac gtg gag gtc agc tgg gaa tac ccc gac acc      720

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IM-5.ST25.txt

Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro	Asp	Thr	
225					230					235					240	
tg	ag	ac	cc	ca	cat	tcc	tac	ttc	tcc	ctg	aca	ttt	tgc	ata	cag	gcc
Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr	Phe	Cys	Ile	Gln	Ala	
				245					250					255		768
cag	ggc	aag	aac	aat	aga	gaa	aag	aaa	gat	aga	ctc	tgc	gtg	gac	aag	
Gln	Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp	Arg	Leu	Cys	Val	Asp	Lys	816
			260					265					270			
acc	tca	gcc	aag	gtc	gtg	tgc	cac	aag	gat	gcc	aag	atc	cgc	gtg	caa	
Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	Ala	Lys	Ile	Arg	Val	Gln	864
		275					280					285				
gcc	cga	gac	cgc	tac	tat	agt	tca	tcc	tg	agc	gac	tg	gca	tct	gtg	
Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser	Asp	Trp	Ala	Ser	Val	912
	290					295					300					
tca	tgc	agt	gg	ggc	gg	ggc	ggc	gga	tct	aga	aac	ttg	cca	acc	cct	
Ser	Cys	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Arg	Asn	Leu	Pro	Thr	Pro	960
305					310					315					320	
act	cca	tcc	ccg	gg	atg	ttc	caa	tgt	ttg	aac	cac	tcc	caa	acc	ttg	
Thr	Pro	Ser	Pro	Gly	Met	Phe	Gln	Cys	Leu	Asn	His	Ser	Gln	Thr	Leu	1008
				325					330					335		
ttg	aga	gcc	gtc	agc	aac	acg	ctt	cag	aag	gcc	aga	caa	act	cta	gaa	
Leu	Arg	Ala	Val	Ser	Asn	Thr	Leu	Gln	Lys	Ala	Arg	Gln	Thr	Leu	Glu	1056
			340					345					350			
tta	tat	tcc	tgc	act	tcc	gaa	gag	att	gat	cat	gaa	gat	atc	aca	aag	
Leu	Tyr	Ser	Cys	Thr	Ser	Glu	Glu	Ile	Asp	His	Glu	Asp	Ile	Thr	Lys	1104
		355					360					365				
gat	aaa	acc	agc	aca	gtg	gag	gcc	tgc	tta	cca	ctg	gaa	tta	acc	atg	
Asp	Lys	Thr	Ser	Thr	Val	Glu	Ala	Cys	Leu	Pro	Leu	Glu	Leu	Thr	Met	1152
	370					375					380					
aat	gag	agt	tgc	ctg	gct	tcc	aga	gag	atc	tct	ttg	ata	act	aac	ggg	
Asn	Glu	Ser	Cys	Leu	Ala	Ser	Arg	Glu	Ile	Ser	Leu	Ile	Thr	Asn	Gly	1200
385					390				395						400	
agt	tgc	ctg	gcc	tct	gga	aag	gcc	tct	ttt	atg	acg	gtc	ctg	tgc	ctt	
Ser	Cys	Leu	Ala	Ser	Gly	Lys	Ala	Ser	Phe	Met	Thr	Val	Leu	Cys	Leu	1248
				405					410					415		
agc	agc	atc	tat	gag	gac	ttg	aag	atg	tac	cag	atg	gaa	ttc	aag	gcc	
Ser	Ser	Ile	Tyr	Glu	Asp	Leu	Lys	Met	Tyr	Gln	Met	Glu	Phe	Lys	Ala	1296
			420					425					430			
atg	aac	gca	aag	ctt	tta	atg	gat	ccc	aag	agg	cag	atc	ttt	ctg	gat	
Met	Asn	Ala	Lys	Leu	Leu	Met	Asp	Pro	Lys	Arg	Gln	Ile	Phe	Leu	Asp	1344
		435					440					445				
caa	aac	atg	ctg	aca	gct	atc	gat	gag	ctg	tta	cag	gcc	ctg	aat	ttc	
Gln	Asn	Met	Leu	Thr	Ala	Ile	Asp	Glu	Leu	Leu	Gln	Ala	Leu	Asn	Phe	1392
	450					455					460					

IM-5.ST25.txt

aac agt gtg act gtg cca cag aaa tcc tcc ctt gaa gag ccg gat ttt 1440
 Asn Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe
 465 470 475 480

tat aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att 1488
 Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile
 485 490 495

cgt gcg gtg acc atc aat aga atg atg tcc tac ttg aac tct tcc 1533
 Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ser Ser
 500 505 510

<210> 67

<211> 511

<212> PRT

<213> Canis familiaris

<400> 67

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Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu
 20 25 30

Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly
 35 40 45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
 50 55 60

Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu
 65 70 75 80

Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
 85 90 95

Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys
 100 105 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr
 115 120 125

Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln
 130 135 140

Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val
 145 150 155 160

IM-5.ST25.txt

Asp	Asn	Arg	Asp	Tyr	Lys	Lys	Tyr	Thr	Val	Glu	Cys	Gln	Glu	Gly	Ser	
				165					170					175		
Ala	Cys	Pro	Ser	Ala	Glu	Glu	Ser	Leu	Pro	Ile	Glu	Val	Val	Val	Asp	
			180					185					190			
Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr	Ser	Ser	Phe	Phe	Ile	
		195					200					205				
Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Thr	Asn	Leu	Gln	Leu	Lys	Pro	
	210					215					220					
Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro	Asp	Thr	
225					230					235					240	
Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr	Phe	Cys	Ile	Gln	Ala	
				245					250					255		
Gln	Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp	Arg	Leu	Cys	Val	Asp	Lys	
			260					265					270			
Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	Ala	Lys	Ile	Arg	Val	Gln	
		275					280					285				
Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser	Asp	Trp	Ala	Ser	Val	
	290					295					300					
Ser	Cys	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Arg	Asn	Leu	Pro	Thr	Pro	
305					310				315						320	
Thr	Pro	Ser	Pro	Gly	Met	Phe	Gln	Cys	Leu	Asn	His	Ser	Gln	Thr	Leu	
				325					330					335		
Leu	Arg	Ala	Val	Ser	Asn	Thr	Leu	Gln	Lys	Ala	Arg	Gln	Thr	Leu	Glu	
			340					345					350			
Leu	Tyr	Ser	Cys	Thr	Ser	Glu	Glu	Ile	Asp	His	Glu	Asp	Ile	Thr	Lys	
		355					360					365				
Asp	Lys	Thr	Ser	Thr	Val	Glu	Ala	Cys	Leu	Pro	Leu	Glu	Leu	Thr	Met	
	370					375					380					
Asn	Glu	Ser	Cys	Leu	Ala	Ser	Arg	Glu	Ile	Ser	Leu	Ile	Thr	Asn	Gly	
385					390					395					400	

IM-5.ST25.txt

Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu
405 410 415

Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala
420 425 430

Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp
435 440 445

Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe
450 455 460

Asn Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe
465 470 475 480

Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile
485 490 495

Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ser Ser
500 505 510

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<212> DNA
<213> Canis familiaris

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ctgtggcaca gtcacactgt tgaaattcag ggcctgtaac agctcatcga tagctgtcag 180
catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240
cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt 300
cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct 360
ggaagccagg caactctcat tcatggttaa ttccagtggc aagcaggcct cactgtgct 420
ggttttatcc tttgtgatat cttcatgatc aatctcttcg gaagtgcagg aatataattc 480
tagagtttgt ctggccttct gaagcgtggt gctgacggct ctcaacaagg tttgggagtg 540
gttcaaacat tggaacatac ccggggatgg agtaggggtt ggcaagtttc tagatccgcc 600
gccaccgcca cactgcatg acacagatgc ccagtcgctc caggatgaac tatagtagcg 660
gtctcgggct tgcacgcgga tcttggcatc cttgtggcac acgaccttgg ctgaggtctt 720

IM-5.ST25.txt

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gtccacgcag agtctatctt tctttctctt attgttcttg cctggggcct gtatgcaaaa 780
tgtraggagg aagtaggaat gtgggggtgct ccagggtgctg gggattccc agctgacctc 840
cacgtgccga gaatttttca atgggttcag ctgcagggtt gtgggtgggt ctggtttgat 900
gatgtctctg atgaagaagc tgctgggtga gttttcatac ttgagcttgt gaatagcatc 960
caccacgacc tcgatgggta ggctctctc ggcagagggg caggcactgc cctcctgaca 1020
ctccactgtg tactttctat aatccctgtt gtccactctg accctctctg ctgaaagtgt 1080
cactgctcca catgtcacc cttgggggtc agagaagcct ctgctacttt tgacactgaa 1140
tttcaaata gtactgattg ccgtcagcca ccagcatgtg aaacgtccag aataattctt 1200
tgctctacat ttcagaaaga tcttattttt ggattctttc tgttccttta agatatcagt 1260
ggaccaaatt ccatcttctt ttttgtgaat caacaggagt gagcggctca gaaccttgcc 1320
tccttttatg caggtatact ggccagcatc tccaaattct ttgacttgga tggtcagagt 1380
tttaccagaa cctaggactt cactgctctg cgtcgaggtc caagtgatgt catcttcttc 1440
aggggtatgg caggtgagga ccaccatttc tccgggggca tcagggtgcc agtccaactc 1500
tacaacataa acatctttct ccagttccca tat 1533

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<210> 69
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<213> Artificial sequence

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<220>
<223> Synthetic Primer

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<400> 69
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<210> 70
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<212> DNA
<213> Artificial sequence

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<220>
<223> Synthetic Primer

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 <210> 72
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 <210> 73
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 <220>
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 aactattgag cacagggata aagatgactg 30

 <210> 74
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 <210> 76
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<220>
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 <400> 76
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 <210> 77
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 <220>
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 <400> 77
 atggccgaca aggtcctgaa ggagaaga 28

 <210> 78
 <211> 33
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 <220>
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 <400> 78
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 <210> 79
 <211> 26
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 <220>
 <223> Synthetic Primer

 <400> 79
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 <210> 80
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 <220>
 <223> Synthetic Primer

 <400> 80
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 <210> 81
 <211> 36
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<213> Artificial sequence
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 <223> Synthetic Primer
 <400> 81
 acaaggatcc accatggccg acaaggatct gaaggg 36

<210> 82
 <211> 39
 <212> DNA
 <213> Artificial sequence
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 <223> Synthetic Primer
 <400> 82
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<210> 83
 <211> 60
 <212> DNA
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 <220>
 <223> Synthetic Primer
 <400> 83
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<210> 84
 <211> 60
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 <213> Artificial sequence
 <220>
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 <400> 84
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<210> 85
 <211> 28
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 <400> 85
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<210> 86
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<212> DNA
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 <220>
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 <400> 86
 tgcaggacac ggatgccag ttgct 25

 <210> 87
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 <400> 87
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 <210> 88
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 <220>
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 <400> 88
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 <210> 89
 <211> 19
 <212> DNA
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 <220>
 <223> Synthetic Primer

 <400> 89
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 <210> 90
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 <400> 90
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 <210> 91

<211> 39
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 <400> 91
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 <220>
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 <400> 92
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<210> 93
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 <212> DNA
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 <220>
 <223> Synthetic Primer

 <400> 93
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<210> 94
 <211> 22
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 <220>
 <223> Synthetic Primer

 <400> 94
 ccatctggta catcttcaag tc 22

<210> 95
 <211> 38
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 <213> Artificial sequence

 <220>
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 <400> 95
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<210> 96
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 <210> 97
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 <212> DNA
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 <223> Synthetic Primer

 <400> 97
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 <210> 98
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 <400> 98
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 <210> 99
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 <400> 99
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 <210> 100
 <211> 29
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 <220>
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 <400> 100
 atctaaatgc atgacacaga tgcccagtc 29

<210> 101
 <211> 561
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(561)

<400> 101
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 Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu Arg Ala Ile
 1 5 10 15

agc aac acg ctt cag aag gcc aga caa act cta gaa ttt tac tcc tgc 96
 Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys
 20 25 30

act tcc gaa gag att gat cat gaa gat atc aca aaa gat aaa acc agc 144
 Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser
 35 40 45

aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat gag agt tgc 192
 Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser Cys
 50 55 60

ctg gct tcc aga gag atc tct ctg ata act aat ggg agt tgc ctg gcc 240
 Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala
 65 70 75 80

tcc aga aag acc tct ttt atg acg acc ctg tgc ctt agc agt atc tat 288
 Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr
 85 90 95

gag gac ttg aag atg tac cag gtg gag ttc aag gcc atg aat gca aag 336
 Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met Asn Ala Lys
 100 105 110

ctg tta atg gat cct aaa agg cag atc ttt ctg gat caa aac atg ctg 384
 Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu
 115 120 125

aca gct att gat gag ctg tta cag gcc ctg aat gtc aac agt gtg act 432
 Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn Ser Val Thr
 130 135 140

gtg cca cag aac tcc tcc ctg gaa gaa ccg gat ttt tat aaa act aaa 480
 Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys
 145 150 155 160

atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt gca gtg acc 528
 Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr
 165 170 175

atc aat aga atg atg agc tat ctg aat gct tcc 561
 Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
 180 185

<210> 102
 <211> 187
 <212> PRT
 <213> Felis catus

<400> 102

Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu Arg Ala Ile
 1 5 10 15

Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys
 20 25 30

Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser
 35 40 45

Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser Cys
 50 55 60

Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala
 65 70 75 80

Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr
 85 90 95

Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met Asn Ala Lys
 100 105 110

Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu
 115 120 125

Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn Ser Val Thr
 130 135 140

Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys
 145 150 155 160

Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr
 165 170 175

Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
 180 185

<210> 103
 <211> 561

<212> DNA

<213> *Felis catus*

<400> 103

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ctgtggcaca gtcacactgt tgacattcag ggccctgtaac agctcatcaa tagctgtcag      180
catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc      240
cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt      300
cataaaagag gtctttctgg aggccaggca actcccatta gttatcagag agatctctct      360
ggaagccagg caactctcat tcatggttaa ttccagtggc aagcaggcct ccactgtgct      420
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<210> 104

<211> 1455

<212> DNA

<213> *Canis familiaris*

<220>

<221> CDS

<222> (232)..(897)

<400> 104

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gcccaattata aaaatgtgac cccccgggtc ggccctccac cgccgcccctc ccctgcccgg      180
tccgcagtcc gcgtccagcg cccgcccgggg tccacgcagc gcccgccag c atg tgc      237
                                         Met Cys
                                         1
ccg ccg cgc ggc ctc ctc ctt gtg acc atc ctg gtc ctg cta agc cac      285
Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu Ser His
          5                      10                      15
ctg gac cac ctt act tgg gcc agg agc ctc ccc aca gcc tca ccg agc      333
Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser Pro Ser
          20                      25                      30
cca gga ata ttc cag tgc ctc aac cac tcc caa aac ctg ctg aga gcc      381
Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu Arg Ala
          35                      40                      45                      50
gtc agc aac acg ctt cag aag gcc aga caa act cta gaa tta tat tcc      429

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IM-5.ST25.txt

Val	Ser	Asn	Thr	Leu	Gln	Lys	Ala	Arg	Gln	Thr	Leu	Glu	Leu	Tyr	Ser		
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Cys	Thr	Ser	Glu	Glu	Ile	Asp	His	Glu	Asp	Ile	Thr	Lys	Asp	Lys	Thr		
			70					75					80				
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Ser	Thr	Val	Glu	Ala	Cys	Leu	Pro	Leu	Glu	Leu	Thr	Met	Asn	Glu	Ser		
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tgc	ctg	gct	tcc	aga	gag	atc	tct	ttg	ata	act	aac	ggg	agt	tgc	ctg	573	
Cys	Leu	Ala	Ser	Arg	Glu	Ile	Ser	Leu	Ile	Thr	Asn	Gly	Ser	Cys	Leu		
	100					105					110						
gcc	tct	gga	aag	gcc	tct	ttt	atg	acg	gtc	ctg	tgc	ctt	agc	agc	atc	621	
Ala	Ser	Gly	Lys	Ala	Ser	Phe	Met	Thr	Val	Leu	Cys	Leu	Ser	Ser	Ile		
115					120				125						130		
tat	gag	gac	ttg	aag	atg	tac	cag	atg	gaa	ttc	aag	gcc	atg	aac	gca	669	
Tyr	Glu	Asp	Leu	Lys	Met	Tyr	Gln	Met	Glu	Phe	Lys	Ala	Met	Asn	Ala		
			135					140						145			
aag	ctt	tta	atg	gat	ccc	aag	agg	cag	atc	ttt	ctg	gat	caa	aac	atg	717	
Lys	Leu	Leu	Met	Asp	Pro	Lys	Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn	Met		
			150				155					160					
ctg	aca	gct	atc	gat	gag	ctg	tta	cag	gcc	ctg	aat	ttc	aac	agt	gtg	765	
Leu	Thr	Ala	Ile	Asp	Glu	Leu	Gln	Ala	Leu	Asn	Phe	Asn	Ser	Val			
		165				170					175						
act	gtg	cca	cag	aaa	tcc	tcc	ctt	gaa	gag	ccg	gat	ttt	tat	aaa	act	813	
Thr	Val	Pro	Gln	Lys	Ser	Ser	Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr		
	180				185					190							
aaa	atc	aag	ctc	tgc	ata	ctt	ctt	cat	gct	ttc	aga	att	cgt	gcg	gtg	861	
Lys	Ile	Lys	Leu	Cys	Ile	Leu	Leu	His	Ala	Phe	Arg	Ile	Arg	Ala	Val		
195				200				205						210			
acc	atc	gat	aga	atg	atg	agt	tat	ctg	aat	tct	tcc	taaaaagctg				907	
Thr	Ile	Asp	Arg	Met	Met	Ser	Tyr	Leu	Asn	Ser	Ser						
			215					220									
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aagatagggg ttaagaacca gggagggggg ggcttgacct ggtcctactt aagctagtag																	1027
gataattctc atgcttggtt acattagttg ccactcaaat tttgaaagat gtgactgtta																	1087
tatccacac gatgcctttg accaagtata tttcacattt actatggata agttaagtgt																	1147
tcgtgagcaa attgctaaag aggaaaaatg tcctcaccga acatgttttt attttccctt																	1207
taatagaaga gcaagacttt ataagctatt tctgtaccaa actgtttgtg gaaacaaaca																	1267
ctcaagcata atttatttaa aaatacttat ttatataatt ttgtgttcat gaaagcatgt																	1327
gaattaatth atatttatth atgttatatt tattaaagta tttattatca agtggatttg																	1387

IM-5.ST25.txt

ggatatctta tgttctaaaa ataaaatgat tgagtagaaa aaaaaaaaaa aaaaaaaaaa 1447

aaaaaaaa 1455

<210> 105

<211> 222

<212> PRT

<213> Canis familiaris

<400> 105

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20 25 30

Pro Ser Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu
35 40 45

Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu
50 55 60

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn
85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser
100 105 110

Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser
115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met
130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn
165 170 175

Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr
180 185 190

IM-5.ST25.txt

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
 195 200 205

Ala Val Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser
 210 215 220

<210> 106
 <211> 1455
 <212> DNA
 <213> Canis familiaris

<400> 106
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 attaatcac atgctttcat gaacacaaaa ttatataaat aagtattttt aaataaatta 180
 tgcttgagtg tttgtttcta caaacagttt ggtacagaaa tagcttataa agtcttgctc 240
 ttctattaaa gggaaaataa aaacatgttc ggtgaggaca tttttcctct ttagcaattt 300
 gctcacgaac acttaactta tccatagtaa atgtgaaata tacttggtca aaggcatcgt 360
 gtgggatata acagtcacat ctttcaaat ttgagtggca actaatgtaa acaagcatga 420
 gaattatcgt actagcttaa gtaggaccag gtcaagccac cccctccctg gttcttaacc 480
 cctatcttat gaaaaattct tttgggttca catttttata ggaatgactt taaagtcgag 540
 agagacctca gctttttagg aagaattcag ataactcatc attctatcga tggtcaccgc 600
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 ctcttcaagg gaggatttct gtggcacagt cacactgttg aaattcaggg cctgtaacag 720
 ctcatcgata gctgtcagca tgttttgatc cagaaagatc tgctcttggt gatccattaa 780
 aagctttgctg ttcattggcct tgaattccat ctggtacatc ttcaagtcct catagatgct 840
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 gacgcgact gcggacgagg caggggaggg cggcggtggg aggccgaccc ggggggtcac 1320

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tttctctctc	tgtctctctc	tacatcagct	tctcggtgac	acgtggagct	gggcccgcg	1440
ggtttgcttc	gtgcc					1455

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<210> 107
<211> 2267
<212> DNA
<213> Canis familiaris
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<220>
<221> CDS
<222> (154) .. (1140)
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[illegible]

IM-5.ST25.txt

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Leu	Lys	Phe	Ser	Val	Lys	Ser	Ser	Arg	Gly	Phe	Ser	Asp	Pro	Gln	Gly	
			155					160					165			
gtg	aca	tgt	gga	gca	gtg	aca	ctt	tca	gca	gag	agg	gtc	aga	gtg	gac	702
Val	Thr	Cys	Gly	Ala	Val	Thr	Leu	Ser	Ala	Glu	Arg	Val	Arg	Val	Asp	
		170					175					180				
aac	agg	gat	tat	aag	aag	tac	aca	gtg	gag	tgt	cag	gag	ggc	agt	gcc	750
Asn	Arg	Asp	Tyr	Lys	Lys	Tyr	Thr	Val	Glu	Cys	Gln	Glu	Gly	Ser	Ala	
	185					190					195					
tgc	ccc	tct	gcc	gag	gag	agc	cta	ccc	atc	gag	gtc	gtg	gtg	gat	gct	798
Cys	Pro	Ser	Ala	Glu	Glu	Ser	Leu	Pro	Ile	Glu	Val	Val	Val	Asp	Ala	
200					205				210						215	
att	cac	aag	ctc	aag	tat	gaa	aac	tac	acc	agc	agc	ttc	ttc	atc	aga	846
Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr	Ser	Ser	Phe	Phe	Ile	Arg	
			220					225						230		
gac	atc	atc	aaa	cca	gac	cca	ccc	aca	aac	ctg	cag	ctg	aag	cca	ttg	894
Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Thr	Asn	Leu	Gln	Leu	Lys	Pro	Leu	
			235					240					245			
aaa	aat	tct	cgg	cac	gtg	gag	gtc	agc	tgg	gaa	tac	ccc	gac	acc	tgg	942
Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro	Asp	Thr	Trp	
		250					255					260				
agc	acc	cca	cat	tcc	tac	ttc	tcc	ctg	aca	ttt	tgc	ata	cag	gcc	cag	990
Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr	Phe	Cys	Ile	Gln	Ala	Gln	
	265					270					275					
ggc	aag	aac	aat	aga	gaa	aag	aaa	gat	aga	ctc	tgc	gtg	gac	aag	acc	1038
Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp	Arg	Leu	Cys	Val	Asp	Lys	Thr	
280					285				290						295	
tca	gcc	aag	gtc	gtg	tgc	cac	aag	gat	gcc	aag	atc	cgc	gtg	caa	gcc	1086
Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	Ala	Lys	Ile	Arg	Val	Gln	Ala	
			300					305						310		
cga	gac	cgc	tac	tat	agt	tca	tcc	tgg	agc	gac	tgg	gca	tct	gtg	tcc	1134
Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser	Asp	Trp	Ala	Ser	Val	Ser	
			315					320					325			
tgc	agt	taggttccac	ccccaggatg	aatcttggag	ggaaagtgga	agatattatg										1190
Cys	Ser															
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IM-5.ST25.txt

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atcatttttta tgacaaccag tgagcacaca atattatgat gccagcacca taatatattt 1610
gtgatggatg ggaacacaga ggtagttaaa tagagacatg gagacacgaa tccatttgag 1670
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tcagaatttc cagctgctcc ttaatagcca ggcaaaaaaa gcacatggat gcaaagaaaa 2030
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tcttgtttgc aataataaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 2267

<210> 108
<211> 329
<212> PRT
<213> Canis familiaris

<400> 108

Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu
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Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val
20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45

Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln
50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val
85 90 95

IM-5.ST25.txt

Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
 100 105 110
 Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
 115 120 125
 Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
 130 135 140
 Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg
 145 150 155 160
 Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser
 165 170 175
 Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
 180 185 190
 Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro
 195 200 205
 Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
 210 215 220
 Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr
 225 230 235 240
 Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
 245 250 255
 Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
 260 265 270
 Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
 275 280 285
 Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
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 Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
 305 310 315 320
 Ser Asp Trp Ala Ser Val Ser Cys Ser
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IM-5.ST25.txt

<210> 109
 <211> 2267
 <212> DNA
 <213> Canis familiaris

<400> 109
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 aatcacttta cagaaagcac attcattact taaaagtagc acctcagcga ttggcacttt 180
 ctgggtcacat ccaccagtca ggttcacttg cgctgtccag taagcaattc ttgaccattt 240
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 ttttttgtgc ttggccatgt tggttctccc tcttgatca taagacctt ttacttccag 360
 acacttacag tgtccctggg tcaactctca atgacttaca gatagatggg gatggggact 420
 ggcaagggtg ctgaagctga atctcaattt gagttatttg tctcaggtct ttctaaattc 480
 aggcatccaa aaactaaact tgcttaaaaa tgcaagtggc cctgaattgc tttatcaaca 540
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 aaatggattc gtgtctccat gtctctattt aactacctct gtgttcccat ccatcacaaa 660
 tatattatgg tgctggcatc ataataattgt gtgctcactg gttgtcataa aaatgatata 720
 ttcttgcttg aaaagttgtc agtataaata acacataaat tcacattttg cataataggg 780
 cctattcctt acagatcagg tcttgagggg atgaaacata caatatatct tggcacacaa 840
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 ggtcagtggc agcctgctag ctgaaaatct ataaataaag tagctgattg tttcagtggg 960
 catttgcatc ttaaagttaa aaaatattgc gaagacacaa taatgaccct ttacaaaaag 1020
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 gtgctccagg tgtcggggta tcccagctg acctccacgt gccgagaatt tttcaatggc 1380
 ttcagctgca ggtttgtggg tgggtctggt ttgatgatgt ctctgatgaa gaagctgctg 1440
 gtgtagtttt catacttgag cttgtgaata gcatccacca cgacctgat gggtaggctc 1500
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<220>
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